

GenCore version 5.1.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 03:46:27 ; Search time 383.692 Seconds  
(without alignments)  
5766.810 Million cell updates/sec

Title: US-10-603-524A-1  
Perfect score: 329  
Sequence: 1 ggtcagcgtgtgcgtgtc.....tgtattaataaatgcttgc 332

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_21.\*  
1: geneseqn1980s.\*  
2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
4: geneseqn2001as.\*  
5: geneseqn2001bs.\*  
6: geneseqn2002as.\*  
7: geneseqn2002bs.\*  
8: geneseqn2003as.\*  
9: geneseqn2003bs.\*  
10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
12: geneseqn2004as.\*  
13: geneseqn2004bs.\*  
14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	329	100.0	332	12 ADI2022	ADI2022 Maize 3'
2	329	100.0	1236	13 ADX30934	Adx30934 Plant ful
3	329	100.0	5118	12 ADP73930	Adp73930 Plasmid p
4	329	100.0	7545	10 ACF58343	Act58343 Nucleotid
5	329	100.0	11643	10 ACF58344	Act58344 Nucleotid
6	329	100.0	13680	12 ADP73931	Adp73931 Plasmid p
7	327.4	99.5	1206	13 ADX61274	Adx61274 Plant ful
8	327.4	99.5	1271	13 ADX10934	Adx10934 Plant ful
9	316.4	96.2	725	13 ADX10594	Adx10594 Plant ful
10	315	95.7	526	13 ADX10536	Adx10536 Plant ful
11	301.4	91.6	1294	13 ADT17732	Adt17732 Plant cdn
12	294	89.4	1057	13 AD083213	Ad083213 Plant ful
13	286	86.9	818	13 ADX65031	Adx65031 Plant ful
14	278.4	84.6	458	13 ADX10617	Adx10617 Plant ful
15	278.4	84.6	1216	13 ADX50588	Adx50588 Plant ful
16	235.4	71.6	594	13 ADX65204	Adx65204 Plant ful
17	232.6	70.7	1234	13 ADX50026	Adx50026 Plant ful
18	232.6	70.7	1278	13 ADX52932	Adx52932 Plant ful
19	204	62.0	1057	13 AD084166	Ad084166 Plant ful

20	91	27.7	1333	2 AAV64064	AAV64064 Zea mays
21	84.8	25.8	758	2 AAV64065	AAV64065 Zea mays
22	81.6	24.8	757	13 ADX60794	Adx60794 Plant ful
23	81.6	24.8	1341	12 ADM47619	Adm47619 Polynucl
24	76.6	23.3	291	10 ABX87875	Abx87875 Corn ear-
25	39	11.9	934	6 ABQ13708	Abq13708 Oligonucl
26	39	11.9	934	6 ABQ13709	Abq13709 Oligonucl
27	38.6	11.7	6380	6 ABN80108	Abn80108 Human che
28	38.4	11.7	15853	6 ABL70466	AbL70466 Chemical
29	38.4	11.7	15853	6 AAS61457	Aas61457 Human gen
30	36.8	11.2	6274	10 ADB54249	Adb54249 Pretreate
31	36.8	11.2	9707	6 ABL33421	AbL33421 Human imm
32	35.6	10.8	478	4 AAL80765	Aal80765 Human pol
33	35.6	10.8	709	6 ABQ48845	Abq48845 Oligonucl
34	35.6	10.8	709	6 ABQ48844	Abq48844 Oligonucl
35	35.6	10.8	2473	14 ADW10450	Adw10450 Colon pro
36	35.6	10.8	6113	6 ABL33823	AbL33823 Human imm
37	35.6	10.8	9299	6 ABL33724	AbL33724 Human imm
38	35.4	10.8	557	13 ADQ54826	Adq54826 Novel can
39	35.4	10.8	1245	13 ADS19123	Ads19123 Rice DNA
40	35.4	10.8	1473	13 ADS47694	Ads47694 Bacterial
41	35.4	10.8	5536	4 AAS46575	Aas46575 Tumour su
42	35.4	10.8	5536	6 ABL33832	AbL33832 Human imm
43	35.4	10.8	6763	4 AAS46488	Aas46488 Tumour su
44	35.4	10.8	6763	6 ABL33555	AbL33555 Human imm
45	35.4	10.8	6763	6 ABL34571	AbL34571 Human met

ALIGNMENTS

RESULT 1  
ADI2022  
ID ADI20222 standard; DNA; 332 BP.  
AC ADI20222;  
XX

DT 22-APR-2004 (first entry)

DE Maize 3' UTR.

XX ss; 3' untranslated region ; UTR; expression cassette ;  
KW transformed plant; promoter ; untranslated leader sequence ;  
KW genetic engineering.

XX Zea mays.

XX WO2004003177-A2.

XX 08-JAN-2004.

XX 25-JUN-2003; 2003WO-US020977.

XX 27-JUN-2002; 2002US-0392571P.

XX (DOWC ) DOW AGROSCIENCES LLC.

XX Cowen NM, Smith KA, Armstrong K;

XX WPI; 2004-071986/07.

XX New isolated DNA molecule useful for genetic engineering of plants or for  
improving the expression of transgenes in plants, particularly corn  
plants.

XX Claim 1; SEQ ID NO 1; 20pp; English.

XX This sequence represents a 3' untranslated region (UTR) which was used in  
the construction of the recombinant expression cassette of the invention.  
XX The expression cassette is for effecting expression of a foreign gene in  
a transformed plant and comprises a promoter operable in plants, an  
XX untranslated leader sequence, a foreign gene of interest, and a 3'UTR.  
XX This cassette may be used to transform plants, for genetic engineering of



OS Zea mays.  
OS Oryza sativa.  
OS Chimeric.  
OS Synthetic.  
OS Unidentified.

XX Key  
FT promoter  
FT 1172..1724  
FT /tag= a  
FT /notes= "Rice actin promoter"  
FT 1727..2281  
FT /tag= b  
FT /product= "Phosphinothricin acyltransferase (PAT)"  
FT 2296..2627  
FT /tag= c  
FT /notes= "Maize lipase 3'UTR. The 3' end of this 3'UTR has  
FT been deduced from that given for pDAB8505 (SEQ ID NO:85),  
FT as the 3'UTR location given for this plasmid is 2296-  
FT 6652"

XX WO2004050838-A2.  
XX  
XX 17-JUN-2004.  
XX  
XX 28-NOV-2003; 2003WO-US037905.  
XX  
XX 27-NOV-2002; 2002US-0429385P.  
XX  
XX (DOWC ) DOW CHEM CO.  
XX (DOWC ) DOW AGROSCIENCES LLC.  
XX (EPIC-) EPICYTE PHARM INC.

XX Briggs K, Glancy T, Hein MB, Hiatt AC, Karnoup AL, Anderson WHK;  
PI Pareddy D, Petolino J, Rubin-Wilson B, Taylor D, Roberts JL;  
XX WPI; 2004-461111/43.  
XX  
XX Novel plant-produced immunoglobulin having glycopeptide or glycan profile  
PT with reduced fucosylation, useful for treating herpes simplex virus  
PT infection.

XX Claim 69; SEQ ID NO 84; 212pp; English.

XX The invention relates to the production of immunoglobulins in plants,  
CC wherein at least a portion of the glycans attached to the immunoglobulins  
CC lack fucose. The immunoglobulins produced can be of any class (i.e., IgG,  
CC IgA, IgM, IgE or IgD) and is especially an anti-herpes simplex virus  
CC (HSV) antibody or an anti-alphaVbeta3, alphaVbeta5 dual integrin  
CC antibody. The invention also relates to constructs, plasmids and vectors  
CC for producing the immunoglobulins; transformed plant cells, calli, plant  
CC tissues and whole plants for producing the immunoglobulins; methods for  
CC producing the immunoglobulins, the immunoglobulins thus produced; and the  
CC use of such immunoglobulins. The immunoglobulins of the invention may be  
CC used to treat HSV infection or tumour angiogenesis. The invention  
CC provides the advantages of antibody production in plants, such as large  
CC scale production, reduced costs, and elimination of pathogenic  
CC contaminants such as viruses and prions, with a simplified (i.e., non-  
CC plant-specific) glycosylation profile which reduces the risk that the  
CC immunoglobulin may not be functional in animals. The present sequence  
CC represents the plasmid pDAB3014, which may be used in the invention. The  
CC plasmid contains a phosphinothricin acyltransferase (PAT) gene under the  
CC control of a rice actin promoter, and a maize lipase 3'UTR.

XX Sequence 5118 BP; 1240 A; 1256 C; 1286 G; 1336 T; 0 U; 0 Other;  
SQ

Query Match 100.0%; Score 329; DB 12; Length 5118;  
Best Local Similarity 99.1%; Pred. No. 2.1e-90;  
Matches 329; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GGTCCGAGCGTGTGCGTCCGTCGTACCTTCGGCCGCGCGCTTCGGCGCGCGATC 60  
2296 GGTCCGAGCGTGTGCGTCCGTCGTACCTTCGGCCGCGCGCTTCGGCGCGCGATC 2355

QY 61 AGAANCCTTGGTGGCGTGTGTGCTTCTGTTTGTCTTAAATTTTACCAAGTTTGT 120  
DB 2356 AGAAGCGTTGGCTTGGCGTGTGTGCTTCTGTTTGTCTTAAATTTTACCAAGTTTGT 2415

QY 121 CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGTCTTTAAANACCCACCGGCACTGGCAGTGA 180  
DB 2416 CAAGGTGGATCGCGTGGTCAAGGCCCGTGTGTCTTTAAAGACCCACCGGCACTGGCAGTGA 2475

QY 181 GTGTTGCTGCTTGTGTAGGCTTTGTGTAGTATGGGCTTTATTTGCTTCTGGATGTTGTGT 240  
DB 2476 GTGTTGCTGCTTGTGTAGGCTTTGTGTAGTATGGGCTTTATTTGCTTCTGGATGTTGTGT 2535

QY 241 ACTACTCTGGTGTGTGAATTTATTTATGATGAGTTCGATTAATTCAGCTGGGCTACC 300  
DB 2536 ACTACTCTGGTGTGTGAATTTATTTATGAGTTCGATTAATTCAGCTGGGCTACC 2595

QY 301 TGGACATTTGTTATGTTATTAATAAATGCTTTGTC 332  
DB 2596 TGGACATTTGTTATGTTATTAATAAATGCTTTGTC 2627

RESULT 4  
ACF58343  
ID ACP58343 standard; DNA; 7545 BP.  
XX  
XX ACP58343;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Nucleotide sequence of plasmid pDAB8504.  
XX  
KW GntIII; N-acetylglucosaminyltransferase; transgenic; glycoprotein; ds.  
XX  
OS Synthetic.  
XX  
XX Key  
FT misc\_feature  
FT 1..1146  
FT /tag= a  
FT /note= "tobacco Rb7 MARs"  
FT 1167..1304  
FT misc\_feature  
FT /tag= b  
FT /note= "linker sequence (ACF58351)"  
FT 1305..2701  
FT promoter  
FT /tag= c  
FT /note= "rice actin promoter and intron"  
FT 2235..2696  
FT intron  
FT /tag= d  
FT /note= "rice actin intron"  
FT 2704..3258  
FT misc\_feature  
FT /tag= e  
FT /note= "PAT gene"  
FT 3259..3272  
FT misc\_feature  
FT /tag= f  
FT /note= "linker sequence (ACF58352)"  
FT 3273..3629  
FT 3'UTR  
FT /tag= g  
FT /note= "maize lipase UTR"  
FT complement(3671..4836)  
FT misc\_feature  
FT /tag= i  
FT /note= "tobacco Rb7 MAR"  
FT 4351..4405  
FT misc\_feature  
FT /tag= h  
FT /note= "linker sequence (ACF58353)"  
FT 4837..4857  
FT misc\_feature  
FT /tag= j  
FT /note= "linker sequence (ACF58354)"  
FT 4858..5103  
FT misc\_feature  
FT /tag= k  
FT /note= "Puc19"  
FT 5104..5130  
FT misc\_feature  
FT /tag= l  
FT /note= "linker sequence (ACF58355)"  
FT 5130..7523  
FT misc\_feature

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FT      /*tag= m
FT      /note= "Puc19"
FT      misc_feature 7524..7545
FT      /*tag= n
FT      /note= "linker sequence (ACF58356)"
XX
XX PN WO2003078614-A2.
XX PD 25-SEP-2003.
XX PF 18-MAR-2003; 2003WO-IB001562.
XX PR 19-MAR-2002; 2002US-0365769P.
XX PR 26-MAR-2002; 2002US-0368047P.
XX PA (PLAN-) PLANT RES INT BV.
XX PI Bakker HAC, Florack DEA, Bosch HJ;
XX DR WPI; 2003-779132/73.
XX PT New plant host cell system for producing a desired glycoprotein comprises
XX PT a mammalian N-acetylglucosaminyltransferase (GnTII) enzyme, a nucleic
XX PT acid sequence encoding the enzyme, or a vector comprising the nucleic
XX PS acid sequence.
XX CC Example 6; Fig 7B; 122pp; English.
XX CC The invention relates to a plant host cell system comprising a mammalian
XX CC UDP-N-acetylglucosamine: beta-D mannose beta(1,4)-N-
XX CC acetylglucosaminyltransferase (GnTII) enzyme, a nucleic acid sequence
XX CC encoding a mammalian GnTII protein, or a vector comprising the GnTII
XX CC nucleic acid. The plant host system is useful in producing a desired
XX CC glycoprotein or its functional fragment. The glycoprotein or its
XX CC functional fragment may be used for the production of a pharmaceutical
XX CC composition. The present sequence represents the nucleotide sequence of
XX CC plasmid pDAB8504
XX SQ Sequence 7545 BP; 2128 A; 1579 C; 1622 G; 2216 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 329; DB 10; Length 7545;
XX Best Local Similarity 99.1%; Pred. No. 2.4e-90;
XX Matches 329; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGTCCAGCGTGTGGTGTCCGTGTGCTTCTGCGCCGCGCGGCTTGGGCGCGATC 60
Db |||||
QY 3273 GGTCCAGCGTGTGGTGTCCGTGTGCTTCTGCGCCGCGCGGCTTGGGCGCGATC 3332
Db |||||
QY 61 AGAANCCTTGGTGTGGTGTGCTTCTGCTTGTCTTAAATTTTACCAGTTTGT 120
Db |||||
QY 3333 AGAAGGTTGCTTGGCGTGTGTGCTTGTGTTTGTCTTAAATTTTACCAGTTTGT 3392
Db |||||
QY 121 CAAGTGGATCCGTTGGTCAAGCCCGTGTGCTTTTAAANACCACCGGCACTGGCAGTGA 180
Db |||||
QY 3393 CAAGGTGGATCCGTTGGTCAAGCCCGTGTGCTTTTAAAGACCCACCGCACTGGCAGTGA 3452
Db |||||
QY 181 GGTGTGCTGTGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 240
Db |||||
QY 3453 GGTGTGCTGTGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 3512
Db |||||
QY 241 ACTACTTGGTGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 300
Db |||||
QY 3513 ACTACTTGGTGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 3572
Db |||||
QY 301 TGGACATTTGTTATGTTAATTAATGCTTTGC 332
Db |||||
QY 3573 TGGACATTTGTTATGTTAATTAATGCTTTGC 3604
Db |||||
XX
XX RESULT 5
XX ACF58344
XX ID ACF58344 standard; DNA; 11643 BP.
XX
```

```
AC ACF58344;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Nucleotide sequence of plasmid pDAB7113.
XX
XX KW GnTII; N-acetylglucosaminyltransferase; transgenic; glycoprotein; ds.
XX
XX OS Synthetic.
XX
XX FH Key
XX FT misc_feature 1..1164
XX FT /tag= a
XX FT /note= "Rb7 MAR v3"
XX FT misc_feature 1165..1233
XX FT /tag= b
XX FT /note= "linker sequence (ACF58357)"
XX FT promoter 1234..3224
XX FT /tag= c
XX FT /note= "maize ubiquitin 1 promoter"
XX FT misc_feature 3225..4891
XX FT /tag= d
XX FT /note= "GnTII v.2"
XX FT 3'UTR 4896..5260
XX FT /tag= e
XX FT /note= "maize peroxidase-5 3'-UTR"
XX FT misc_feature 5261..5404
XX FT /tag= f
XX FT /note= "multiple cloning sites (ACF58358)"
XX FT promoter 5405..6802
XX FT /tag= g
XX FT /note= "rice actin 1 promoter v2"
XX FT misc_feature 6803..7358
XX FT /tag= h
XX FT /note= "PAT v3"
XX FT misc_feature 7359..7372
XX FT /tag= i
XX FT /note= "linker sequence (ACF58359)"
XX FT 3'UTR 7373..7729
XX FT /tag= j
XX FT /note= "maize lipase UTR"
XX FT misc_feature 7730..7770
XX FT /tag= k
XX FT /note= "linker sequence (ACF58360)"
XX FT misc_feature 7771..8934
XX FT /tag= l
XX FT /note= "Rb7 MAR v3"
XX FT misc_feature 8935..11643
XX FT /tag= m
XX FT /note= "Puc19"
XX FT misc_feature 10164..11021
XX FT /tag= n
XX FT /note= "ampicillin resistance gene"
XX
XX WO2003078614-A2.
XX
XX 25-SEP-2003.
XX
XX 18-MAR-2003; 2003WO-IB001562.
XX
XX 19-MAR-2002; 2002US-0365769P.
XX
XX 26-MAR-2002; 2002US-0368047P.
XX
XX (PLAN-) PLANT RES INT BV.
XX
XX Bakker HAC, Florack DEA, Bosch HJ;
XX
XX WPI; 2003-779132/73.
XX
XX New plant host cell system for producing a desired glycoprotein comprises
XX a mammalian N-acetylglucosaminyltransferase (GnTII) enzyme, a nucleic
XX acid sequence encoding the enzyme, or a vector comprising the nucleic
XX acid sequence.
```



XX Claim 69; SEQ ID NO 85; 212pp; English.

XX CC The invention relates to the production of immunoglobulins in plants,

XX CC wherein at least a portion of the glycans attached to the immunoglobulins

XX CC lack fucose. The immunoglobulins produced can be of any class (i.e., IgG,

XX CC IgA, IgM, IgG or IgD) and is especially an anti-herpes simplex virus

XX CC (HSV) antibody or an anti-alpha/beta3, alpha/beta5 dual integrin

XX CC antibody. The invention also relates to constructed, plasmids and vectors

XX CC for producing the immunoglobulins; transformed plant cells, calli, plant

XX CC tissues and whole plants for producing the immunoglobulins; methods for

XX CC producing the immunoglobulins, the immunoglobulins thus produced; and the

XX CC use of such immunoglobulins. The immunoglobulins of the invention may be

XX CC used to treat HSV infection or tumour angiogenesis. The invention

XX CC provides the advantages of antibody production in plants, such as large

XX CC scale production, reduced costs, and elimination of pathogenic

XX CC contaminants such as viruses and prions, with a simplified (i.e., non-

XX CC plant-specific) glycosylation profile which reduces the risk that the

XX CC immunoglobulin may not be functional in animals. The present sequence

XX CC represents the plasmid pAB8505, which contains codon optimised DNA

XX CC sequences encoding the heavy and light chains of the human anti-HSV1/HSV2

XX CC monoclonal IgA antibody HX8 each of which are fused to mouse leader

XX CC sequences. Both heavy and light chain fusion genes are under the control

XX CC of maize endosperm-specific gamma-zinn promoters. The plasmid also

XX CC contains a phosphinothricin acyltransferase (PAT) gene under the control

XX CC of a rice actin promoter.

XX SQ Sequence 13680 BP; 3886 A; 3069 C; 2934 G; 3788 T; 0 U; 3 Other;

Query Match 100.0%; Score 329; DB 12; Length 13680;

Best Local Similarity 100.0%; Pred. No. 3.1e-90;

Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCGACGGTGGCGTCCGTCGTACGTTCTGCGCGCGCGCTTGGCGCGCATC 60

DB 9831 GGTCCGACGGTGGCGTCCGTCGTACGTTCTGCGCGCGCGCTTGGCGCGCATC 9890

QY 61 AGAAGCGTTGCGTGGCGTGGTGGTCTGCTTCTGCTTTGCTTTAAATTTACCAAGTTTGGTT 120

DB 9891 AGAAGCGTTGCGTGGCGTGGTGGTCTGCTTCTGCTTTGCTTTAAATTTACCAAGTTTGGTT 9950

QY 121 CAAGGTGGATCGCGTGGTCAAGCCCGTGGTCTTTAAANACCACCGGCATCGGACGTGA 180

DB 9951 CAAGGTGGATCGCGTGGTCAAGCCCGTGGTCTTTAAANACCACCGGCATCGGACGTGA 10010

QY 181 GTGTCGTCGTTGCTGAGGCTTTGGTACGTATGGGCTTTATTGCTTCGAGTCTGCTGT 240

DB 10011 GTGTCGTCGTTGCTGAGGCTTTGGTACGTATGGGCTTTATTGCTTCGAGTCTGCTGT 10070

QY 241 ACTACTTGGGTTTGGTTGAATTATTATGANCAGTTCGTTATTTGTAATTCAGTCTGGCTACC 300

DB 10071 ACTACTTGGGTTTGGTTGAATTATTATGANCAGTTCGTTATTTGTAATTCAGTCTGGCTACC 10130

QY 301 TGGACATTGTTATGTTATTAATAATGCTTTGC 332

DB 10131 TGGACATTGTTATGTTATTAATAATGCTTTGC 10162

RESULT 7

ID ADX61274

XX ADX61274 standard; cDNA; 1206 BP.

XX AC ADX61274;

XX AC ADX61274;

XX DT 21-APR-2005 (first entry)

XX DE Plant full length insert polynucleotide seqid 32117.

XX KW plant protectant; plant growth regulant; gene therapy; plant;

XX KW recombinant DNA construct; physical array; plant breeding marker;

XX KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

XX KW extreme osmotic condition; pathogen tolerance; pest tolerance;

XX KW growth rate; cell cycle pathway; disease resistance;

XX KW

salactomannan production; lignin production; plant growth regulator;

yield; plant growth; plant development; seed oil; protein yield;

protein content; gene; ss.

Unidentified.

US2004034888-A1.

19-FEB-2004.

28-APR-2003; 2003US-00425114.

06-MAY-1999; 99US-00304517.

05-NOV-2001; 2001US-00985678.

(LIU/) LIU J.

(ZHOU/) ZHOU Y.

(KOVA/) KOVALIC D K.

(SCRE/) SCREEN S E.

(TABA/) TABASKA J E.

(CAOV/) CAO Y.

LIU J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

WPI; 2004-180133/17.

New recombinant DNA construct, useful for improving plant tolerance to

cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or

pests, for conferring increased resistance to plant disease, or for

improving yield.

Claim 1; SEQ ID NO 32117; 15pp; English.

The invention describes a recombinant DNA construct comprising a

polynucleotide consisting of a sequence encoding an amino acid sequence

available in electronic form from the US patent office at

ftp.segdata.ustpo.gov/sequence.html?DocID:2004034888. The polynucleotide

of the invention are also useful in physical arrays of molecules and as

plant breeding markers. The recombinant DNA construct is useful for

improving plant tolerance to cold, heat, drought, herbicides, extreme

osmotic conditions, pathogens or pests, for manipulating growth rate in

plant cells by modification of the cell cycle pathway, for conferring

increased resistance to plant disease, for producing galactomannan,

lignin or plant growth regulators, for increasing the rate of homologous

recombination in plants, for improving yield by modification of

photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

or by providing improved plant growth and development under at least one

stress condition or for modifying seed oil or protein yield and/or

content. This sequence represents a plant full length insert

polynucleotide that can be used in the recombinant DNA construct of the

invention.

Sequence 1206 BP; 281 A; 337 C; 395 G; 193 T; 0 U; 0 Other;

Query Match 99.5%; Score 327.4; DB 13; Length 1206;

Best Local Similarity 98.8%; Pred. No. 3.6e-90;

Matches 328; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGTCCGACGGTGGTGGTCCGTCGTACGTTCTGCGCGCGCGGCTTGGCGCGCATC 60

DB 867 GGTCCGACGGTGGTGGTCCGTCGTACGTTCTGCGCGCGCGGCTTGGCGCGCATC 926

QY 61 AGAAGCGTTGCGTGGCGTGGTGGTCTGCTTCTGCTTTAAATTTACCAAGTTTGGTT 120

DB 927 AGAAGCGTTGCGTGGCGTGGTGGTCTGCTTCTGCTTTAAATTTACCAAGTTTGGTT 986

QY 121 CAAGGTGGATCGCGTGGTCAAGGCGCGCTGCTTTAAANACCACCGGCATCGGACGTGA 180

DB 987 CAAGGTGGATCGCGTGGTCAAGGCGCGCTGCTTTAAANACCACCGGCATCGGACGTGA 1046

QY 181 GTGTCGTCGTTGTTAGGCTTTGGTACGTATGGGCTTTATTGCTTCTCGATGTTGTTGT 240

DB 1047 GTGTCGTCGTTGTTAGGCTTTGGTACGTATGGGCTTTATTGCTTCTCGATGTTGTTGT 1106

QY 241 ACTACTGGGTTGGTGAATTATATGACAGTTGGCTATTGTAATTCAGCTGGGCTACC 300  
 |||||  
 Db 1107 ACTACTGGGTTGGTGAATTATATGACAGTTGGCTATTGTAATTCAGCTGGGCTACC 1166  
 |||||  
 QY 301 TGGACATTGTTATGTAATTAATAAATGCTTTGC 332  
 |||||  
 Db 1167 TGGACATTGTTATGTAATTAATAAATGCTTTGC 1198  
 |||||

## RESULT 8

ADX10934  
 ID ADX10934 standard; cDNA; 1271 BP.

AC ADX10934;

DT 21-APR-2005 (first entry)

XX Plant full length insert polynucleotide seqid 5509.

XX plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content; gene; ss.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIUJ/) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D K.

XX (SCRE/) SCREEN S E.

XX (TABA/) TABASKA J E.

XX (CAOY/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.

XX Claim 1; SEQ ID NO 5509; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or

CC content. This sequence represents a plant full length insert  
 CC polynucleotide that can be used in the recombinant DNA construct of the  
 CC invention.

XX Sequence 1271 BP; 295 A; 350 C; 412 G; 214 T; 0 U; 0 Other;

XX Query Match 99.5%; Score 327.4; DB 13; Length 1271;

XX Best Local Similarity 98.8%; Pred. No. 3.7e-90;

XX Matches 328; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGTCCGAGCGTGTGGCTGTCCTGCTACGTTCTGCGCGCGCGGCTTGGGCGCGGATC 60  
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Db 932 GGTCCGAGCGTGTGGCTGTCCTGCTACGTTCTGCGCGCGCGGCTTGGGCGCGGATC 991  
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QY 61 AGAANCCTTGGCTTGGCGGTGTGCTTCTGCTTAAATTTTACCAAGTTTGT 120  
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Db 992 AGAAGCGTTGCGTGTGGCGGTGTGCTTCTGCTTAAATTTTACCAAGTTTGT 1051  
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QY 121 CAAGGTGATCGCGTGTCAAGGCCGCTGCTTTAAACCCACCGGCACTGGCAGTGA 180  
 |||||

Db 1052 CAAGGTGATCGCGTGTCAAGGCCGCTGCTTTAAAGACCCACCGGCACTGGCAGTGA 1111  
 |||||

QY 181 GGTGTGCTGCTTGTGTAGCTTTGCTATGCTTATTTGCTTCTGGAATGTTGCT 240  
 |||||

Db 1112 GGTGTGCTGCTTGTGTAGCTTTGCTATGCTTATTTGCTTCTGGAATGTTGCT 1171  
 |||||

QY 241 ACTACTTGGGTTTGTGTAATTATTATGACAGTTGCGTATTGTAATTCAGCTGGGCTACC 300  
 |||||

Db 1172 ACTACTTGGGTTTGTGTAATTATTATGACAGTTGCGTATTGTAATTCAGCTGGGCTACC 1231  
 |||||

QY 301 TGGACATTGTTATGTAATTAATAAATGCTTTGC 332  
 |||||

Db 1232 TGGACATTGTTATGTAATTAATAAATGCTTTGC 1263  
 |||||

## RESULT 9

ADX10594

ID ADX10594 standard; cDNA; 725 BP.

XX AC ADX10594;

XX 21-APR-2005 (first entry)

XX Plant full length insert polynucleotide seqid 5169.

XX plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content; gene; ss.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIUJ/) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D K.

XX (SCRE/) SCREEN S E.

XX (TABA/) TABASKA J E.

XX (CAOY/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

```
XX WPI; 2004-180133/17.
DR
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 5169; 15pp; English.
PS
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 725 BP; 149 A; 205 C; 226 G; 145 T; 0 U; 0 Other;
Query Match 96.2%; Score 316.4; DB 13; Length 725;
Best Local Similarity 98.8%; Pred. No. 7.2e-87;
Matches 317; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGTCCAGCGTGTGGTGTCCGTCTGCTAGCTTCTGCGCGCGCGGCTTTGGGCGCGCATC 60
DB 405 GGTCCAGCGTGTGGTGTCCGTCTGCTAGCTTCTGCGCGCGCGGCTTTGGGCGCGCATC 464
QY 61 AGAANCCTTGGCTTGGCGTGTGTGCTTCTGCTTCTTAATTTTACCAAGTTTGT 120
DB 465 AGAAGCGTTGGCTTGGCGTGTGTGCTTCTGCTTCTTAATTTTACCAAGTTTGT 524
QY 121 CAAGGTGATCGCGTGTCAAGGCGCGTGTCTTAAANACCCAGCCGACCTGGCAGTGA 180
DB 525 CAAGGTGATCGCGTGTCAAGGCGCGTGTCTTAAANACCCAGCCGACCTGGCAGTGA 584
QY 181 GTGTTGCTGTGTGTAGGCTTTGTAGCTATGAGGCTTTATTTGCTTCTGATGTTGT 240
DB 585 GTGTTGCTGTGTGTAGGCTTTGTAGCTATGAGGCTTTATTTGCTTCTGATGTTGT 644
QY 241 ACTACTGGGTTTGTGTAATTAATGANCAGTTCGCTATGTAATTCAGCTGGGCTACC 300
DB 645 ACTACTGGGTTTGTGTAATTAATGAGCAGTTCGCTATGTAATTCAGCTGGGCTACC 704
QY 301 TGGACATTTGTTATGTAATTAAT 321
DB 705 TGGACATTTGTTATGTAATTAAT 725
RESULT 10
ADX10536
ID ADX10536 standard; cDNA; 526 BP.
XX
AC ADX10536;
DB
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 5111.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
```

```
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PP 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
XX (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 5111; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 526 BP; 95 A; 134 C; 169 G; 128 T; 0 U; 0 Other;
Query Match 95.7%; Score 315; DB 13; Length 526;
Best Local Similarity 99.1%; Pred. No. 1.7e-86;
Matches 315; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGTCCAGCGTGTGGTGTCCGTCTGCTAGCTTCTGCGCGCGCGGCTTTGGGCGCGCATC 60
DB 209 GGTCCAGCGTGTGGTGTCCGTCTGCTAGCTTCTGCGCGCGCGGCTTTGGGCGCGCATC 268
QY 61 AGAANCCTTGGCTTGGCGTGTGTGCTTCTGCTTCTTAATTTTACCAAGTTTGT 120
DB 269 AGAAGCGTTGGCTTGGCGTGTGTGCTTCTGCTTCTTAATTTTACCAAGTTTGT 328
QY 121 CAAGGTGATCGCGTGTCAAGGCGCGTGTGCTTTAAANACCCAGCCGACCTGGCAGTGA 180
DB 329 CAAGGTGATCGCGTGTCAAGGCGCGTGTGCTTTAAAGAGCCACCGGACCTGGCAGTGA 388
QY 181 GTGTTGCTGTGTGTAGGCTTTGTCGATGAGGCTTTATTTGCTTCTGATGTTGT 240
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Db 389 GTGTCCTGCTGTAGCTTGGTACGTATGGGCTTTATTTGCTTCTGGAATGTGT 448  
 QY 241 ACTACTTGGGTTTGTGAATATTATGANCAGTTGGTATTGTAATTCAGTGGGCTACC 300  
 Db 449 ACTACTTGGGTTTGTGAATATTATGAGCAGTTGGTATTGTAATTCAGTGGGCTACC 508  
 QY 301 TGGACATTCGTATGTATT 318  
 Db 509 TGGACATTCGTATGTATT 526

## RESULT 11

ADT17732  
 ID ADT17732 standard; cDNA; 1294 BP.

XX AC

XX ADT17732;

XX 13-JAN-2005 (first entry)

XX DE Plant cDNA, Seq ID 3058.

XX KW Plant; ss; gene; transgenic; cold tolerance; growth rate;  
 KW drought tolerance; disease resistance; galactomannan production;  
 KW plant growth regulator; heat tolerance; herbicide tolerance;  
 KW lignin production; extreme osmotic condition tolerance;  
 KW pathogens resistance; pest resistance; yield improvement; seed oil yield;  
 KW seed protein yield.

XX OS Viridiplantae.

XX PN US2004216190-A1.

XX PD 28-OCT-2004.

XX PF 18-DEC-2003; 2003US-00739930.

XX PR 28-APR-2003; 2003US-00424599.

XX PS 28-APR-2003; 2003US-00425115.

XX PA (KOVA/) KOVALIC D K.

XX PI Kovalic DK;

XX DR WPI; 2004-757369/74.

XX PT New recombinant DNA constructs useful in the field of biochemistry and  
 PT genetics, and in particular for producing transgenic plants with improved  
 PT biological characteristics.

XX PS Claim 1; SEQ ID NO 3058; 14pp; English.

XX CC The invention relates a recombinant DNA construct comprising a  
 CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:  
 CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences  
 CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,  
 CC Arabidopsis, wheat and rape but the specification does not indicate which  
 CC sequences is derived from which organism. Also included is a method of  
 CC producing a plant having an improved property, comprising transforming a  
 CC plant with a recombinant DNA construct comprising a promoter region  
 CC functional in a plant cell operably joined to a polynucleotide encoding a  
 CC polypeptide associated with the property, and growing the transformed  
 CC plant. The property is selected from improving plant cold tolerance, for  
 CC manipulating growth rate in plant cells by modification of the cell cycle  
 CC pathway, for improving plant drought tolerance, for providing increased  
 CC resistance to plant disease, for galactomannan production, for production  
 CC of plant growth regulators, for improving plant heat tolerance, for  
 CC improving plant tolerance to herbicides, for increasing the rate of  
 CC homologous recombination in plants, for lignin production, for improving  
 CC plant tolerance to extreme osmotic conditions, for improving plant  
 CC tolerance to pathogens or pests, for yield improvement by modification of  
 CC photosynthesis, for modifying seed oil yield and/or content, for  
 CC modifying seed protein yield and/or content, for yield improvement by

CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC and for yield improvement by providing improved plant growth and  
 CC development under at least one stress condition. The polynucleotide may  
 CC also encode a plant transcription factor. The methods and compositions of  
 CC the present invention are useful in the field of biochemistry and  
 CC genetics, in particular for producing transgenic plants with improved  
 CC biological characteristics such as increased yield, improved nitrogen  
 CC flow, increasing plant tolerance to cold or heat, improving plant  
 CC tolerance to extreme osmotic and drought conditions, and improving plant  
 CC tolerance to plant pests or pathogens. They can also be used in physical  
 CC arrays of molecules, plant breeding markers, computer-based storage and  
 CC analysis systems. The present sequence is one of the 5544 plant cDNA  
 CC sequences of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20040216190.

XX SQ Sequence 1294 BP; 307 A; 351 C; 418 G; 214 T; 0 U; 4 Other;

Query Match 91.6%; Score 301.4; DB 13; Length 1294;

Best Local Similarity 97.0%; Pred. No. 3.8e-82;

Matches 326; Conservative 1; Mismatches 5; Indels 4; Gaps 2;

QY 1 GGTCCAGCGCTGTC-GTGTCCGTGCTAGCTTCTGCGCGCGCGGCC---TTGGGGCGGC 56

Db 951 GGTCCAGCGCTGTCGGGTGTCGTGCTAGCTTCTGCGCGCGCGGCCCTTATTGGGGCGGC 1010

QY 57 GATCAGAACGTTGGTTGGGTGGTGTGCTGCTTCTGTTTGTCTTAATTTTACCAAGTTT 116

Db 1011 GATCAGAACGTTGGTTGGGTGGTGTGCTTCTGTTTGTCTTAATTTTACCAAGTTT 1070

QY 117 GTTTCAGGTGGATCGGTGTCGTCGCTGTCGCTGCTTCTTAANACCCACCGCCTGGCA 176

Db 1071 GTTTCAGGTGGATCGGTGTCGTCGCTGTCGCTGCTTCTTAANACCCACCGCCTGGCA 1130

QY 177 GTGAGTGTGCTGCTTGTGTTAGGCTTGTGCTAGTATGGCTTATTGCTTCTGATGTT 236

Db 1131 GTGAGTGTGCTGCTTGTGTTAGGCTTGTGCTAGTATGGCTTATTGCTTCTGATGTT 1190

QY 237 GTGTACTACTTGGGTTTGTGTAATTTATTCANCAAGTTGCGTATTGTAATTCAGCTGGC 296

Db 1191 GTGTACTACTTGGGTTTGTGTAATTTATTCANCAAGTTGCGTATTGTAATTCAGCTGGC 1250

QY 297 TACCTGGACATTTGTTATGTTATTAATAATGCTTTGC 332

Db 1251 TACCTGGACATTTGTTATGTTATTAATAATGCTTTGC 1286

## RESULT 12

AD083213

ID AD083213 standard; cDNA; 1057 BP.

XX AC

XX AD083213;

XX DT 21-APR-2005 (first entry)

XX DE Plant full length insert polynucleotide seqid 1933.

XX KW plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content; gene; ss.

XX OS Unidentified.

XX PN US2004034888-A1.

XX PD 19-FEB-2004.





PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAS/) TABASKA J E.  
PA (CAOY/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
DR  
XX  
XX  
PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
XX  
PS Claim 1; SEQ ID NO 25328; 15pp; English.  
XX  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 1216 BP; 282 A; 342 C; 402 G; 190 T; 0 U; 0 Other;  
Query Match 84.6%; Score 278.4; DB 13; Length 1216;  
Best Local Similarity 98.6%; Pred. No. 4.4e-75;  
Matches 279; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GGTGCGAGCGTGTGGTGTGCGTGTGCGTGTGCGCGCGCGCTTGGCGCGCGATC 60  
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QY 61 AGAANGTTGCGTGTGGCGTGTGCGTGTGCGTGTGCTTTAATTTTACCAAGTTTGT 120  
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QY 994 AGAAGCGTTGCGTGTGGCGTGTGCGTGTGCGTGTGCTTTAATTTTACCAAGTTTGT 1053  
Db |||||  
QY 121 CAAGGTGGATCGCGTGTCAAGCGCGTGTGCTTTTAAANACCCACCGGCACTGGCAGTGA 180  
Db |||||  
QY 1054 CAAGGTGGATCGCGTGTCAAGGTCCGTGTGCTTTTAAAGACCCACCGGCACTGGCAGTGA 1113  
Db |||||  
QY 181 GGTGTCGCTGTGTGAGCGTTTGGTGTGAGTGTGCTTTATTTGCTTCTGGATGTTGT 240  
Db |||||  
QY 1114 GTGTCGCTGTGTGAGCGTTTGGTGTGAGTGTGCTTTATTTGCTTCTGGATGTTGT 1173  
Db |||||  
QY 241 ACTACTTGGGTTTGTGTAATTATTATGANCAGTTGCTATTGT 283  
Db |||||  
QY 1174 ACTACTTGGGTTTGTGTAATTATTATGAGCAGTTGCGTATTGT 1216  
Db |||||

Search completed: March 8, 2006, 04:18:51  
Job time : 386.692 secs



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QY	301	TGGACATTGTTATGTATTATAAATGCTTTGC	332
Db	3573	TGGACATTGTTATGTATTATAAATGCTTTGC	3604
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LOCUS		AX840289	linear PAT 16-DEC-2003
DEFINITION		AX840289	synthetic construct
ACCESSION		AX840289.1	GI:39978688
VERSION			other sequences; artificial sequences.
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			Bakker, H.A., Florack, D.E. and Bosch, H.J.
TITLE			GntIII (udp-n-acetylglucosamine-beta-D mannose
JOURNAL			beta(1,4)-n-acetylglucosaminyltransferase iii) expression in plants
FEATURES			Patent: WO 03078614-A 11 25-SEP-2003;
source			Plant Research International B.V. (NL)
			Location/Qualifiers
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Query Match		100.0%; Score 329; DB 6; Length 11643;	
Best Local Similarity		99.1%; Pred. No. 2.7e-82;	
Matches 329; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
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QY	61	AGAANGCTTCGGTTGGCGTGTGTGCTCTCTGTTTTGCTTTTAATTTTACCACGTTTGT	120
Db	7433	AGAAGCGTTCCGTTGGCGTGTGTGCTCTCTGTTTTGCTTTTAATTTTACCACGTTTGT	7492
QY	121	CAAGGTGGATCGCGTGTCAAAGCCCCGTGTGCTTTTAAANA CCCACGGCACTGGCAGTGA	180
Db	7493	CAAGGTGGATCGCGTGTCAAAGCCCCGTGTGCTTTTAAAGACCCACCGGCACCTGGCAGTGA	7552
QY	181	GTGTTGCTTGTGTGTAGGCTTTGGTAGCATATGGGCTTTAATTTGCTTCTGGATGTTGTGT	240
Db	7553	GTGTTGCTTGTGTGTAGGCTTTGGTAGCATATGGGCTTTAATTTGCTTCTGGATGTTGTGT	7612
QY	241	ACTACTTTGGGTTTGTTGAATTATTATGANCAGTTGGGTATTGTAAATTCAGCTGGGCTACC	300
Db	7613	ACTACTTTGGGTTTGTTGAATTATTATGACAGTTGGGTATTGTAAATTCAGCTGGGCTACC	7672
QY	301	TGGACATTGTTATGTATTATAAATGCTTTGC	332
Db	7673	TGGACATTGTTATGTATTATAAATGCTTTGC	7704
RESULT 3			
MZELIPASE			
LOCUS			linear PLN 01-MAY-2001
DEFINITION		Zea mays dehydrin (dhn-2) mRNA, complete cds.	
ACCESSION		L35913	
VERSION		L35913.1	GI:532622
KEYWORDS			
SOURCE			Zea mays

KEYWORDS FLI CDNA.  
 SOURCE Zea mays  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 722)  
 AUTHORS Lai, J., Dey, N., Kim, C.-S., Bharti, A.K., Rudd, S., Mayer, K.F.X., Larkins, B., Becraft, P. and Messing, J.  
 TITLE Characterization of the maize endosperm transcriptome and its comparison to the rice genome  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 722)  
 AUTHORS Lai, J., Dey, N., Kim, C.-S., Bharti, A.K., Rudd, S., Mayer, K.F.X., Larkins, B., Becraft, P. and Messing, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-OCT-2004) Waksman Institute, Rutgers University, 190 Frelinghuysen Rd, Piscataway, NJ 08854, USA  
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 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4577"  
 /clone="Contig566.P"  
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 Query Match 89.2%; Score 293.4; DB 15; Length 722;  
 Best Local Similarity 98.7%; Pred. No. 3e-72;  
 Matches 294; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 GGTCCAGCGTGTGGTGTCCGTGACGTTCTGCGCGCGCGGCTTGGGCGCGGATC 60  
 DB 410 GGTCCAGCGTGTGGTGTCCGTGACGTTCTGCGCGCGCGGCTTGGGCGCGGATC 469  
 QY 61 AGAAGCGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 120  
 DB 470 AGAAGCGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 529  
 QY 121 CAAGTGATGCGGTGGTCAAGCGCGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 180  
 DB 530 CAAGTGATGCGGTGGTCAAGCGCGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 589  
 QY 181 GTGTGTGCTGT 240  
 DB 590 GTGTGTGCTGT 649  
 QY 241 ACTACTGGGT 298  
 DB 650 ACTACTGGGT 707  
 RESULT 5  
 AR059010  
 LOCUS AR059010 1333 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 1 from patent US 5837848.  
 ACCESSION AR059010  
 VERSION AR059010.1 GI:5984587  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 1333)  
 AUTHORS Ely, S., Evans, I. Jeffrey, and Schuch, W. Walter.  
 TITLE Root-specific promoter  
 JOURNAL Patent: US 5837848-A 1 17-NOV-1998;  
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 source 1..1333  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 ORIGIN  
 Query Match 27.7%; Score 91; DB 6; Length 1333;  
 Best Local Similarity 64.7%; Pred. No. 9.5e-15;  
 Matches 211; Conservative 0; Mismatches 83; Indels 32; Gaps 4;  
 QY 22 GTGTGTGCTGT 81  
 DB 995 GTGTGTGCTGT 1054  
 QY 82 GTGTGTGCTGT 139  
 DB 1055 GTGTGTGCTGT 1114  
 QY 140 AAGGCCCGTGTGCTTTA-----AANACCCACCGGCACCTGGCAGTGAGTGTGTGTGTGT 193  
 DB 1115 AAGTCCCGTGTGCTTATTAAGTGGATGCGGTGACTTGGCAGTGAGTGTGTGTGTGT 1174  
 QY 194 TGTAGGCTTTGGTACGTATGGGCTTTATTTGCTTCTCGA-----232  
 DB 1175 TGTAGGCTGTGTACGTACGTACGGGCTTTATTTGGTCCCAAGTCAAAAGTCACGGTGGTCT 1234  
 QY 233 TGTGTGTACTACTGTGGT 292  
 DB 1235 GGATGTTGTGTACTTGGGTTTGTGA---ATTATGAGCAGCTGCGTGTGTGTGTGTGTGT 1291  
 QY 293 GGGCTACCTGACCATTTGTATGTATT 318  
 DB 1292 GGGCTACCTGATGCGGTTAATAATT 1317  
 RESULT 6  
 BD272350  
 LOCUS BD272350 1333 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Root-specific promoter.  
 ACCESSION BD272350  
 VERSION BD272350.1 GI:33082118  
 KEYWORDS JP 2002537760-A/1.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 1333)  
 AUTHORS Ely, S., Evans, I.J. and Schuch, W.W.  
 TITLE Root-specific promoter  
 JOURNAL Patent: JP 2002537760-A 1 12-NOV-2002;  
 ADVANTA TECHNOLOGY LTD  
 COMMENT OS Zea mays (maize)  
 PN JP 2002537760-A/1  
 PD 12-NOV-2002  
 PF 16-NOV-1998 JP 2000582576  
 PI SUSAN ELY, IAN JEFFREY EVANS, WOLFGANG WALTER SCHUCH PC  
 C12N15/09,C12N5/10//A01H5/00,C12N15/00,C12N5/00 CC a, c, t, g,  
 other or unknown  
 CC a, c, t, g, other or unknown  
 CC a, c, t, g, other or unknown  
 FH Key Location/Qualifiers  
 FT modified base (139)  
 FT modified base (582)  
 FT modified base (588).  
 FEATURES Location/Qualifiers  
 source 1..1333  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4577"  
 ORIGIN  
 Query Match 27.7%; Score 91; DB 6; Length 1333;  
 Best Local Similarity 64.7%; Pred. No. 9.5e-15;  
 Matches 211; Conservative 0; Mismatches 83; Indels 32; Gaps 4;  
 QY 22 GTGTGTGCTGT 81  
 DB 995 GTGTGTGCTGT 1054  
 QY 82 GTGTGTGCTGT 139

1055 TGTGTTGGTCTGCTGTTGCTTTTACAAAGTTTCTTTCAAGTGGATCGCTGCTC 1114  
QY 140 AAGCCCGTGTCTTTA-----AANACCACCGCACTGCGAGTGTGCTGCTTG 193  
Db 1115 AAGTCCGTGTCTCTATTAAAGTGGATCGGCTGACTGCGAGTGTGCTGCTTG 1174  
QY 194 TGTAGCTTTGGTACGTATGGCTTTATTGCTTCTGGA----- 232  
Db 1175 TGTAGGACGTGTACGTACGGCTTTATTGTTGCCAAGTCAAAAGTCAGGTGCTGCT 1234  
QY 233 TGTGTGTACTGTTGGTGTGTTGAAATTATTATGANCAGTTGCGTATTGTAATTCAGCT 292  
Db 1235 GGTATGTTGTGTACTGTTGGTGTGTTGGA---ATTATGAGCAGTGTGCTGTTGTAATTCGCT 1291  
QY 293 GGGTACCTGACCATGTTATGTAAT 318  
Db 1292 GGGTACCTGATGCGGTTAATAAT 1317

RESULT 7  
AR059011/c AR059011 758 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 2 from patent US 5837848.  
DEFINITION AR059011  
ACCESSION AR059011  
VERSION AR059011.1 GI:5984588  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 758)  
AUTHORS Ely,S., Evans,I.Jeffrey. and Schuch,W.Walter.  
TITLE Root-specific promoter  
JOURNAL Patent: US 5837848-A 2 17-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..758  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 25.8%; Score 84.8; DB 6; Length 758;  
Best Local Similarity 68.2%; Pred. No. 5.3e-13;  
Matches 202; Conservative 0; Mismatches 61; Indels 33; Gaps 5;  
QY 38 GCGCGGCTTGGCGCGGATCAGAACGTTGCGTGGTGTGCTGCTTCTGCTTCTGCTT 97  
Db 440 GTCTTGGCGGCTGCGCGGATAGAACG-TAGCTAGCGTTGGCATGTGTGTTGGTTCT 382  
QY 98 CTTTAATTTTACC--AAGTTTGTTCAGGTGGATCGGTGGTCAAGCCCGTGTGCTTT 155  
Db 381 GTTTCCTTTTACAAAGTTTGTTCAGGTGGATCGGTGGTCAAGTCCGTGTGCTTCT 322  
QY 156 AAANAC-----CCACCGGCACTGCGAGTGTGCTGCTGTAGGCTTTGGTACG 209  
Db 321 ATTAAGTGGATCGGTGACTCTGCGAGTGTGCTGCTGTGTAGGACGTGTGCTACG 262  
QY 210 TATGGCTTTATTGCTTCTGGA-----TGTGTGTACTACTTG 248  
Db 261 TACGGCTTTATTGTTGGTCCCAAGTCAAAAGTCACGTCGGTCTGGATGTTGTGTACTTG 202  
QY 249 GGTGTTGTAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACTCGA 304  
Db 201 GGTGTTGTTGA---ATTATGAGCAGCTGCGTGTGTTGTAATTCGGCTGGGCTACTCGA 149

RESULT 8  
BD272351/c BD272351 758 bp DNA linear PAT 17-JUL-2003  
LOCUS Root-specific promoter.  
DEFINITION BD272351  
ACCESSION BD272351  
VERSION BD272351.1 GI:33082119  
KEYWORDS JP 2002537760-A/2.  
SOURCE Zea mays

ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 758)  
AUTHORS Ely,S., Evans,I.J. and Schuch,W.W.  
TITLE Root-specific promoter  
JOURNAL Patent: JP 2002537760-A 2 12-NOV-2002;  
COMMENT ADVANTA TECHNOLOGY LTD  
OS Zea mays (maize)  
PN JP 2002537760-A/2  
PD 12-NOV-2002  
PF 16-NOV-1998 JP 2000582576  
PI SUSAN ELY IAN JEFFREY EVANS WOLFGANG WALTER SCHUCH PC  
C12N15/09,C12N5/10/A01H5/00,C12N15/00,C12N5/00 CC a, c, t, g,  
other or unknown  
CC a, c, t, g, other or unknown  
CC a, c, t, g, other or unknown  
FH Key Location/Qualifiers  
FT modified\_base (429)  
FT modified\_base (486)..(488)  
FT modified\_base (490).  
FEATURES Location/Qualifiers  
source 1..758  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4577"

ORIGIN  
Query Match 25.8%; Score 84.8; DB 6; Length 758;  
Best Local Similarity 68.2%; Pred. No. 5.3e-13;  
Matches 202; Conservative 0; Mismatches 61; Indels 33; Gaps 5;  
QY 38 GCGCGGCTTGGCGCGGATCAGAACGTTGCGTGGTGTGCTGCTTCTGCTTCTGCTT 97  
Db 440 GTCTTGGCGGCTGCGCGGATAGAACG-TAGCTAGCGTTGGCATGTGTGTTGGTTCT 382  
QY 98 CTTTAATTTTACC--AAGTTTGTTCAGGTGGATCGGTGGTCAAGCCCGTGTGCTTT 155  
Db 381 GTTTCCTTTTACAAAGTTTGTTCAGGTGGATCGGTGGTCAAGTCCGTGTGCTTCT 322  
QY 156 AAANAC-----CCACCGGCACTGCGAGTGTGCTGCTGTAGGCTTTGGTACG 209  
Db 321 ATTAAGTGGATCGGTGACTCTGCGAGTGTGCTGCTGTGTAGGACGTGTGCTACG 262  
QY 210 TATGGCTTTATTGCTTCTGGA-----TGTGTGTACTACTTG 248  
Db 261 TACGGCTTTATTGTTGGTCCCAAGTCAAAAGTCACGTCGGTCTGGATGTTGTGTACTTG 202  
QY 249 GGTGTTGTAATTATTATGANCAGTTGCGTATTGTAATTCAGCTGGGCTACTCGA 304  
Db 201 GGTGTTGTTGA---ATTATGAGCAGCTGCGTGTGTTGTAATTCGGCTGGGCTACTCGA 149

RESULT 9  
AR250976 AR250976 291 bp DNA linear PAT 20-DEC-2002  
LOCUS Sequence 6335 from patent US 6476212.  
DEFINITION AR250976  
ACCESSION AR250976  
VERSION AR250976.1 GI:27298850  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 291)  
AUTHORS Lalgudi,R.V., Ito,L.Y. and Sherman,B.K.  
TITLE Polynucleotides and polypeptides derived from corn ear  
JOURNAL Patent: US 6476212-A 6335 05-NOV-2002;  
INCYTE Genomics, Inc.; Palo Alto, CA  
FEATURES Location/Qualifiers  
source 1..291  
/organism="unknown"  
/mol\_type="genomic DNA"





Genomic DNA amplification  
RedTaq (Sigma)  
Sequencing buffer  
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 40 48 34 37 40 40 40 37 42 42 51 56  
56 56 56 47 42 42 43 42 37 40 40 40 40 37 40 35 30 42 42  
43 56 56 56 88 90 70 66 56 55 56 78 77 74 76 84 90 90 86  
86 80 74 69 71 60 60 57 57 69 76 78 81 90 90 90 90 90 90  
84 84 56 45 45 28 28 28 42 40 45 87 89 82 74 77 77 77 73  
77 79 90 90 81 81 81 81 77 90 86 85 74 74 82 79 75 77 80 80  
82 90 85 72 72 72 72 72 77 75 88 88 90 80 80 80 85 85 90  
90 90 80 83 89 78 83 84 79 79 85 85 90 89 83 86 82 82 82  
83 90 80 89 80 82 69 71 81 78 84 84 84 77 77 71 73 73 83  
83 88 90 80 78 74 76 76 77 65 57 55 60 57 61 54 71 69 40 40  
40 56 22 22 22 22 56 47 47 42 42 42 56 47 56 40 40 40 48.

## FEATURES

Location/Qualifiers

1..233

/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73(2)"  
/db\_xref="taxon:4577"  
/clone\_lib="Zea mays B73(2)"  
/dev\_stage="seedling"  
/note="Organ: leaf; genomic DNA from inbred line"

## STS

<1..>233

## ORIGIN

Query Match 22.1%; Score 72.8; DB 10; Length 233;  
Best Local Similarity 67.1%; Pred. No. 1.3e-09;  
Matches 141; Conservative 0; Mismatches 49; Indels 20; Gaps 2;  
QY 115 TTGTTTCAAGTGGATCGGTCGAGCCGCTGCTTTAAANACCACCGGC---AC 171  
Db 1 TTGTTTCAAGTGGATCGGTCGAGCCGCTGCTTTAAAGTGGATCGGTCGAC 60  
QY 172 TGGCAGTCAGTGTCTGCTGTGTAGGCTTTGGTACGTATGGGCTTTATTGCTTCTGG 231  
Db 61 TGGCAGTCAGTGTCTGCTGTGTAGGCTTTGGTACGTATGGGCTTTATTGCTTCTCA 120  
QY 232 ATGTTGTGTACTACTTGGGTTTG-----TTGAATTATTATGANCAGTT 274  
Db 121 AGTCAAAAGTCACGGTCGGTCTGGATGTTGTACTGCGTTTGTGAATTATGACAGCT 180  
QY 275 GCGTATTGTAATTCAGCTGGGCTACCTGGA 304  
Db 181 GCGGCTTGTAAATTCGGCTGGGCTACCTGGA 210

## RESULT 12

BV106711  
LOCUS PZA01565 Ky21 Zea mays Ky21 Zea mays STS 13-MAR-2004  
DEFINITION 233 bp DNA linear STS genomic, sequence tagged site.

ACCESSION BV106711

VERSION BV106711.1 GI:45422666

KEYWORDS STS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

1 (bases 1 to 233)

MPZ-UCI Joint SNP Discovery

Unpublished (2003)

COMMENT

Contact: Brandon S. Gaut

Dept. Ecology and Evolutionary Biology

U.C. Irvine

321 Steinhaus Hall, Irvine, CA 92697-2525, USA

Tel: (949) 824-2564

Fax: (949) 824-2181

Email: bgaut@uci.edu  
Primer A: ACCAAAAGTTTGTTCACAGTGGA  
Primer B: TTTTGGGAGAAACCAAGC  
STS size: 233

## Protocol:

PCR amplification of genomic DNA

Template: 50 ng

Primer: each 0.5 uM

dNTPs: each 200 uM

Taq Polymerase: RedTaq (Sigma)

Total Vol: 10 ul

Amplicon sequencing

ABI protocol - using d-Rhodamine terminator cycle

sequencing ready reaction with amplitaq DNA polymerase FS

Sequence ran on ABI 3700 sequencer.

## Buffer:

Genomic DNA amplification

RedTaq (Sigma)

Sequencing buffer

d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 36 40 40 32 37 40 40 35 40 40 40 46  
40 42 42 42 42 42 28 28 37 37 37 50 50 50 52 39 44 43 60 59  
64 69 71 77 80 77 60 55 55 50 58 69 74 69 74 74 82 90 88 82 79  
77 77 74 72 73 64 59 57 57 64 75 73 80 80 84 90 90 90 90 90  
77 80 80 82 81 76 57 60 52 86 81 77 77 78 73 72 72 72 72 72  
75 85 86 90 90 81 82 78 77 77 90 86 85 74 74 82 85 76 80 84 84  
84 90 90 77 70 70 70 70 72 80 80 90 90 90 90 82 82 77 77 77 90  
84 86 90 80 88 86 78 75 80 80 75 80 90 90 88 90 83 86 82 82 82  
86 90 90 86 90 70 70 74 79 78 80 82 80 74 76 73 72 71 84 85 87  
87 85 90 85 90 78 81 77 90 78 66 58 57 61 57 57 56 74 74 45 45  
45 56 24 24 24 24 56 56 56 47 42 42 56 56 56 40 40 46 40 40 37 40.

## FEATURES

Location/Qualifiers

1..233

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="Ky21"

/db\_xref="taxon:4577"

/clone\_lib="Zea mays Ky21"

/dev\_stage="seedling"

/note="Organ: leaf; genomic DNA from inbred line"

<1..>233

## STS

## ORIGIN

Query Match 22.1%; Score 72.8; DB 10; Length 233;  
Best Local Similarity 67.1%; Pred. No. 1.3e-09;  
Matches 141; Conservative 0; Mismatches 49; Indels 20; Gaps 2;  
QY 115 TTGTTTCAAGTGGATCGGTCGAGCCGCTGCTTTAAANACCACCGGC---AC 171  
Db 1 TTGTTTCAAGTGGATCGGTCGAGCCGCTGCTTTAAAGTGGATCGGTCGAC 60  
QY 172 TGGCAGTCAGTGTCTGCTGTGTAGGCTTTGGTACGTATGGGCTTTATTGCTTCTGG 231  
Db 61 TGGCAGTCAGTGTCTGCTGTGTAGGCTTTGGTACGTATGGGCTTTATTGCTTCTCA 120  
QY 232 ATGTTGTGTACTACTTGGGTTTG-----TTGAATTATTATGANCAGTT 274  
Db 121 AGTCAAAAGTCACGGTCGGTCTGGATGTTGTACTGCGTTTGTGAATTATGACAGCT 180  
QY 275 GCGTATTGTAATTCAGCTGGGCTACCTGGA 304  
Db 181 GCGGCTTGTAAATTCGGCTGGGCTACCTGGA 210

## RESULT 13

BV079992

LOCUS

DEFINITION

tagged site.

ACCESSION BV079992

VERSION BV079992.1 GI:37051649

237 bp DNA linear STS 30-SEP-2003

sc1186 p5 I114H Zea mays I114H Zea mays STS genomic, sequence





GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 04:07:00 ; Search time 2667.19 Seconds  
(without alignments)  
5823.847 Million cell updates/sec

Title: US-10-603-524A-1  
Perfect score: 329  
Sequence: 1 ggtcgacggtgctgctgc.....tgtattaataaatgctttgc 332

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_est3:  
4: gb\_hc:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est7:  
9: gb\_gss1:  
10: gb\_gss2:  
11: gb\_gss3:

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	327.4	99.5	519	3	BM382021
C 2	327.4	99.5	559	3	BM381414
C 3	327.4	99.5	615	1	AI649488
C 4	327.4	99.5	615	8	DN204249
C 5	327.4	99.5	660	6	CF629927
C 6	327.4	99.5	675	8	DN212434
C 7	327.4	99.5	753	8	DR955206
C 8	327.4	99.5	782	9	CC700159
C 9	325.8	99.0	444	7	CN844293
C 10	325.8	99.0	603	7	CN827377
C 11	324.2	98.5	412	6	CF633415
C 12	321.8	97.8	443	7	CN844286
C 13	319.4	97.1	434	2	BG841223
C 14	313.4	95.3	629	6	CF625618
C 15	311.6	94.7	449	6	CB380309
C 16	311.2	94.6	687	8	DN232860
C 17	303.4	92.2	618	8	DN232769
C 18	286.4	87.1	330	6	DN828411
C 19	283.4	85.1	490	6	CF626006
C 20	283.4	85.1	568	6	CF628060
C 21	279.6	85.0	634	1	AI629748
C 22	278.4	84.6	524	6	CF629847

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C 23	278.4	84.6	665	6	CF625636
C 24	278.4	84.6	745	7	CK985786
C 25	278.4	84.6	1256	4	AY111114
C 26	278.4	84.5	605	8	DN221053
C 27	275.6	83.8	461	8	DN210598
C 28	274.4	83.4	294	6	CB381621
C 29	274.4	83.4	518	1	AI586566
C 30	270.6	82.2	521	3	BM379174
C 31	270.4	82.2	637	6	CD001819
C 32	270.2	82.1	794	9	CC700174
C 33	266.4	81.0	549	6	CD484944
C 34	264.4	80.4	594	6	CD573321
C 35	258.4	78.5	305	7	CV071480
C 36	253.8	77.1	588	3	BM382407
C 37	241	73.3	266	6	CB351546
C 38	237.8	72.3	273	7	CN845511
C 39	237.4	72.2	559	3	BM337639
C 40	237.4	72.2	586	3	BM379625
C 41	232.6	70.7	434	6	CF057128
C 42	232.6	70.7	491	5	BQ486909
C 43	231	70.2	432	6	CF057584
C 44	223.4	67.9	696	3	BM334944
C 45	221.6	67.4	611	3	BM339531

ALIGNMENTS

RESULT 1  
BM382021/c

LOCUS BM382021 519 bp mRNA linear EST 16-JAN-2002

DEFINITION MEST543-E03.univ ISUM6 Zea mays cdna clone MEST543-E03 3', mRNA sequence.

ACCESSION BM382021 GI:18180811

VERSION BM382021.1

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 519)  
Wen, J.F., Qiu, F., Guo, L., Ashlock, D.A and Schnable, P.S.  
Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones  
Unpublished (2001)

JOURNAL

COMMENT  
Contact: Patrick S. Schnable  
Schnable Laboratory  
Iowa State University  
2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA  
Tel: 515-294-0975  
Fax: 515-294-5256  
Email: schnable@iastate.edu  
Individual basecall and confidence value were assigned using the Phred software (http://www.phrap.org/). Overall sequence quality assessment and vector trimming was conducted using the Lucy software (version 1.16s, http://www.tigr.org/softlab/). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high quality region of each sequence. Low-quality bases between the poly-r and the high-quality region were replaced with N's to serve as spacers using a Perl program (est\_process.pl), written by Dr. Hui-Hsien Chou.

PCR Primers  
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)  
BACKWARD: primer Sp6 (ATT TAG GTG ACA CTA TAG)  
Seq primer: universal (GTA AAA CGA CGG CCA GT)  
POLYA-Yes.

FEATURES  
Location/Qualifiers  
1..519  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"



Seedling stressed root cDNA library from Wang/Bohnert lab"

increasingly stressed from many/volunteer

Matches	328	Conservative	0	Mismatches	4	Indels	0	Gaps	0
---------	-----	--------------	---	------------	---	--------	---	------	---

Qy	61	AGAACGTTGGCTTGGCGTGTGTGCTCTGCTTAAATTTTACCAAGTTGTTT	120
Db	288	AGAAGCGTTGGCGTGTGTGCTCTGCTTAAATTTTACCAAGTTGTTT	229
Qy	121	CAAGGTGGATCGCGTGGTCAAGGCCGCTGTCTTTAAANACCCACGGGCACTGGCAGTGA	180
Db	228	CAAGGTGGATCGCGTGGTCAAGGTCGCTGTCTTTAAAGACCACCGGCACCTGGCAGTGA	169
Qy	181	GTGTTGCTGCTGTGTGATGAGCTTTGGTACGTAACGGGCTTTATTTGCTTCTGGATGTTGTGT	240
Db	168	GTGTTGCTGCTGTGTGAGGCTTTGGTACGTAACGGGCTTTATTTGCTTCTGGATGTTGTGT	109
Qy	241	ACTACTTGGGTTGTTTGAATTATTATGANCAGTTGGGTATTGTAATTCAGCTGGGCTACC	300
Db	108	ACTACTTGGGTTGTTTGAATTATTATGACGAGTTGGGTATTGTAATTCAGCTGGGCTACC	49
Qy	301	TGGACATTGTTATGTATTAAATAAAGCTTTGC	332
Db	48	TGGACATTGTTATGTATTAAATAAAGCTTTGC	17

## RESULT 4

LOCUS	DN204249	615 bp	linear	EST 28-FEB-2005
DEFINITION	MEST001_F08.T7-1 UGA-ZmsAM-XZ2 204249 mRNA			
ACCESSION	MEST001_F08.T7-1 UGA-ZmsAM-XZ2 204249			
VERSION	DN204249.1 GI:60337276			
KEYWORDS	EST			

**SOURCE**  
**ORGANISM**

REFERENCE  
Chen, H.D., Zhang, X., Zhou, R. L., Arias, L. A. C., Shendelman, J. M., Zaubovits, N., Borsuk, L. A., Emrich, S. J., Ashlock, D. A., Scanlon, M. J., and Schnable, P. S.  
1 (bases 1 to 615)  
Expressed Sequence Tags from Arabidopsis Maize Shoot Apical Meristems  
TITLE

**TITLE**

Unpublished (2004)  
Contact: Patrick S. Schnable  
Schnable Laboratory  
Iowa State University  
2035B R.J. Carver CO-Lab, Ames, IA 50011-3650, USA  
Tel: 515-294-0975  
Fax: 515-294-5256  
Email: [schnable@iastate.edu](mailto:schnable@iastate.edu)  
Location/Qualifiers  
1 615

## FEATURES

## Source





Inserts ranged from ~0.5kb to >2.5 kb, as determined by PCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites that flank the cloned cDNA inserts. The purified PCR products, representing the entire cDNA population cloned in each library, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 300C.

Non-hybridized single-stranded DNA circles were separated from hybridized DNA representing partially double-stranded and electrophoretized into DH10B. The total number of clones with insert was: zmrws05: 2.0x10<sup>7</sup>; zmrws48: 4.2x10<sup>7</sup>; zmrw00: 1.1x10<sup>7</sup>. The background of empty clones was less than 2%.

Insert size, determined by PCR of the entire library, ranged from 0.5kb to 2.5kb. (1) Sharp R B; Silk W K; Hsiao T C. Growth of the Maize Primary Root at Low Water Potentials I. Spatial Distribution of Expansive Growth. Plant Physiology (Rockville). 87(1). 1988. 50-57. (2) Spollen W G; Leubner M E; Samuels T D; Bernstein N; Sharp R E. Abscissic acid accumulation maintains maize primary root elongation at low water potentials by restricting ethylene production. Plant Physiology (Rockville). 122(3). March, 2000. 967-976.

TAG TISSUE=Root segment 3

Db	118	ACTACTTTGGGTTTCTTGAATTTATTATGACGACGTTTGCATTATTGTAATTCAGCTGGGCTACC	59
Qy	301	TGGACATTGTTATGCTATTATAAATGCTTTGC	332
Db	58	TGGACATTGTTATGCTATTATAAATGCTTTGC	27
RESULT 7			
DR955206/c			
LOCUS	DR955206	753 bp	mrna
DEFINITION	ZM BF50049D21.f_ZM_BFB Zea mays cDNA 3', mRNA sequence.		linear EST 03-AUG-2005
ACCESSION	DR955206		
VERSION	DR955206.1	GI:71757269	
KEYWORDS	EST.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 753)		
AUTHORS	Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.		
TITLE	Maize Full-length cDNA Project		
JOURNAL	Unpublished (2005)		
COMMENT	Contact: Yeisoo Yu		

Forbes Building, Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9585  
Fax: 520 621 1259  
Email: yeisoo@genome.arizona.edu  
Plate: 0049 row: D column: 21.  
Location/Qualifiers  
1. .753  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="mixed (silks, husks, ears, pollen, shoot  
tips, leaf, root tips, whole seed, embryo)"  
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/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM BFB"  
/note=Vector: pCMV-SPORT 6.1; Site\_1: EcoRV; Site\_2:  
NotI; Maize Full length cDNA library (3530 library)  
created by Invitrogen from multiple tissues; Organ: silks,  
husks, ears, pollen, shoot tips, leaf, root tips, whole  
seed, embryo. This is a Gateway compatible vector.

ORIGIN

99.5%; Score 327.4; DB 8; Length 753;

Query Match

permitted clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A) + mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for a selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 mm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>). "



normalized cDNA libraries. Dark-grown maize seedlings with primary roots 12–20 mm in length were transplanted to high water potential (–0.03 MPa) or low water potential (–1.6 MPa) vermiculite, and harvested at 5 h and 48 h after transplanting. About 1,000 roots were used for each of the low water potential libraries (zmrw505 and zmrw548) while 500 roots were combined from each of the two time points at high water potential (zmrw000). Each root was divided into 4 segments (distances are from the junction of the root apex and root cap): segment 1, 0–3 mm plus the root cap; segment 2, 3–7 mm; segment 3, 7–12 mm; segment 4, 12–20 mm. (For details of conditions see (1) with nutrient modifications as in (2)). The three normalized cDNA libraries were constructed in the lab of Hans Bonbert (University of Illinois-UC). Total RNA was extracted by the 'hot phenol' method (Plant Molecular Biology manual, D5: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/A280). Poly(A)<sup>+</sup>mRNA was isolated twice from total RNA using the Oligotex Direct mRNA kit (Qiagen). Poly(A)<sup>+</sup> mRNA was converted to double-stranded cDNA and tagged by using modified Oligo(dT) primers. One of 4 sequence tags corresponding to a different segment of the root was added to the 3'-end of the modified Oligo(dT) primers, including a NotI site and used to reverse transcribe the segment-specific mRNAs into cDNAs. Each library contains all four tags. A suffix (s1, s2, s3, or s4) has been added to each sequence identifier to designate which region of the root (root segment\_1, 2, 3, or 4) the sequence was found in based on the identification of the tag. A suffix of 80 indicates that the sequence tag, and hence the source segment, could not be identified. The double stranded cDNAs were size-selected (>450 bp). Size selected cDNAs were adapted with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene) and electroporated into *E. coli* DH10B. The total number of white colony forming units (cfu) in the primary libraries before amplification was as follows: zmrw505: 3.37 x 10<sup>6</sup>; zmrw548: 4.87 x 10<sup>6</sup>; zmrw000: 3 x 10<sup>6</sup>. The background of empty clones was less than 1%. Inserts ranged from ~0.5kb to >2.5 kb, as determined by PCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites that flank the cloned cDNA inserts. The purified PCR products, representing the entire cDNA population cloned in each library, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 4 hours at 300C. Non-hybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B. The total number of clones with insert was: zmrw505: 2.0x10<sup>7</sup>; zmrw548: 4.2x10<sup>7</sup>; zmrw000: 1.1x10<sup>7</sup>. The background of empty clones was less than 2%. Insert size, determined by PCR of the entire library, ranged from 0.5kb to 2.5kb. (1) Sharp R E; Silk W K; Hsiao T C. Growth of the Maize Primary Root at Low Water Potentials I. Spatial Distribution of Expansive Growth. Plant Physiology (Rockville). 87(1), 1988. 50-57. (2) Spollen W G; LeNoble M E; Samuels T D; Bernstein N; Sharp R E. Abscissic acid accumulation maintains maize primary root elongation at low water potentials by restricting ethylene production. Plant Physiology (Rockville). 122(3). March, 2000. 967-976. TAG TSSUE=Not found TAG SEQ=Not found

## ORIGIN

Query Match 99.0%; Score 325.8; DB 7; Length 603;  
Best Local Similarity 98.5%; Pred. No. 1.9e-81;

Matches	327;	Conservative	0;	Mismatches	5;	Indels	0;	Gaps	0;
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QY	61	AGAACGTTTCCGTTGCGGTGTGTGTCTTCTGTTTGTCTTTAATTTTACCAAGTTTGT	120						
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QY	121	CAAGTGTGATTCGCGTGTCAAGCCCGTGTCTTTAAANACCCACCGGCACTGGCAGTGA	180						
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QY	181	GTGTTCTCTCTGTGTAGCGTTTGTGTACGTATGGGCTTTATTGTCTTCTGGATTTGTGT	240						
Db	160	GTGTTCTCTCTGTGTAGCGTTTGTGTACGTATGGGCTTTATTGTCTTCTGGATTTGTGT	101						
QY	241	ACTACTTGGGTTTGTGTGAATTTATTATGANCAGTTGCGTATTGTAAATTCAGCTGGGCTACC	300						
Db	100	ACTACTTGGGTTTGTGTGAATTTATTATGAGCAGTTGCGTATTGTAAATTCAGCTGGGCTACC	41						
QY	301	TGGACATTGTATGTATTAAATAAATCCTTTGC	332						
Db	40	TGGACATTGTATGTATTAAATAAATCCTTAGC	9						
RESULT 11									
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LOCUS	CF633415	zmrws48_0B20-015-f03.s3	zmrws48	Zea mays	cdNA 3', mRNA	linear	EST 02-OCT-2003		
DEFINITION	CF633415								
ACCESSION	CF633415.1	GI:37392332							
VERSION	EST.								
KEYWORDS									
SOURCE	Zea mays								
ORGANISM	Zea mays								
REFERENCE									
AUTHORS	Bohner, H., Sharp, R.E., Springer, G.K., Poroyko, V., Fredricksen, M., Sharp, L.G., Spollen, W.G., Ries, J., Guillen, A., Khambat, A., Topinka, C., Davis, G.E., Schachman, D., Wu, Y. and Nguyen, H.T.								
TITLE	NSF Grant DBI-0211842; Functional Genomics of Root Growth and Root Signaling Under Drought								
JOURNAL	Unpublished (2003)								
COMMENT	Contact: Hans Bohner University of Illinois, Urbana-Champaign 1201 West Gregory Drive, Urbana, IL 61801, USA Tel: 217-265-5475 Fax: 217-333-5574 Email: bohnerth@life.uiuc.edu POLYA=Yes.								

**FEATURES**  
**SOURCE**

`/organism="Zea mays"`  
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`/db_xref="taxon:4577"`  
`/clone_lib="zmrws48"`  
`/note="Samples were collected in Robert E. Sharp's lab (University of Missouri-Columbia) to construct three normalized cDNA libraries. Dark-grown maize seedlings with primary roots 12-20 mm in length were transplanted to high (~0.03 MPa) or low water potential (-1.6 MPa) vermiculite, and harvested at 5 h and 48 h after transplanting. About 1,000 roots were used for each of the low water potential libraries (zmrws05 and zmrws48) while 500 roots were combined from each of the two time points at high water potential (zmrw00). Each root was divided into 4 segments (distances are from the junction of the root apex and root cap): segment 1, 0-3 mm plus the root cap; segment 2, 3-7 mm; segment 3, 7-12 mm; segment 4, 12-20 mm. [For details of conditions see (1) with nutrient modifications as in`

(2)). The three normalized cDNA libraries were constructed in the lab of Hans Bonmert (University of Illinois-UC). Total RNA was extracted by the 'hot Phenol' method (Plant Molecular Biology manual, D5: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/280). Poly(A)+mRNA was isolated twice from total RNA using the Oligotex Direct mRNA kit (Qiagen). Poly(A)+mRNA was converted to double-stranded cDNA and tagged by using modified Oligo(dT) primers. One of 4 sequence tags corresponding to a different segment of the root was added to the 3'-end of the modified Oligo(dT) primers, including a NotI site and used to reverse transcribe the segment-specific mRNAs into cDNAs. Each library contains all four tags. A suffix (s1, s2, s3, or s4) has been added to each sequence identifier to designate which region of the root (Root segment 1, 2, 3, or 4) the sequence was found in based on the Identification of the tag. A suffix of s0 indicates that the sequence tag, and hence the source segment, could not be identified. The double stranded cDNAs were size-selected (>450 bp). Size selected cDNAs were adaptorized with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene) and electroporated into E.coli DH10B. The total number of white colony forming units (CFU) in the primary libraries before amplification was as follows: zmrw05: 3.37 x 106; zmrw48: 4.87 x 106; zmrw00: 3 x 106. The background of empty clones was less than 1%. Inserts ranged from ~0.5kb to >2.5 kb, as determined by PCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites that flank the cloned cDNA inserts. The purified PCR products, representing the entire cDNA population cloned in each library, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 300C. Non-hybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B. The total number of clones with insert was: zmrw05: 2.0x107; zmrw48: 4.2x107; zmrw00: 1.1x107. The background of empty clones was less than 2%. Insert size, determined by PCR of the entire library, ranged from 0.5kb to 2.5kb. (1) Sharp R E; Silk W K; Hsiao T C. Growth of the Maize Primary Root at Low Water Potentials I. Spatial Distribution of Expansive Growth. Plant Physiology (Rockville). 87(1). 1988. 50-57. (2) Spollen W G; LeNoble M E; Samuels T D; Bernstein N; Sharp R E. Absciscic acid accumulation maintains maize primary root elongation at low water potentials by restricting ethylene production. Plant Physiology (Rockville). 122 (3). March, 2000. 967-976. TAG TISSUE=Root\_segment\_3 TAG SBO=TCGCA"

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LOCUS   BG841223
DEFINITION MEST19-A06.T3 ISUM4-TN Zea mays cDNA clone MEST19-A06 3', mRNA
sequence.
ACCESSION BG841223
VERSION   BG841223.2 GI:14243593
KEYWORDS EST.
SOURCE   Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 434)
Qiu,F., Cui,F., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings and Silks
Unpublished (2001)
On May 25, 2001 this sequence version replaced gi:14207545.
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA
Tel: 515-294-0975
Fax: 515-294-5256
Email: schnable@iastate.edu
PCR Primers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
FEATURES
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/mol_type="mRNA"
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/clone_lib="ISUM4-TN"
/note="Vector: pT7T3PAC; Site 1: EcoRI; Site 2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5'
AACTGGAAGATTCCGCGCGCAGGAATTTTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT7T3PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."
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## ORIGIN

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Query Match          97.1%; Score 319.4; DB 2; Length 434;
Best Local Similarity 98.8%; Pred. No. 1.2e-79;
Matches 320; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      121 CAAGGTGATCGCGTGTGTCGAGGCCGCTGTCTTTAAANACCCACCGGCACTGGCAGTGA 180
Db      231 CAAGGTGATCGCGTGTGTCGAGGTCCTGTGCTTTAAAGACCCACCGGCACTGGCAGTGA 290
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LOCUS   CF625618
DEFINITION zmrws05_0A21-002-h12.s4 zmrws05 Zea mays cDNA 3', mRNA sequence.
ACCESSION CF625618
VERSION   CF625618.1 GI:37377941
KEYWORDS EST.
SOURCE   Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 629)
Bohnert,H., Sharp,R.E., Springer,G.K., Poroyko,V., Fredricksen,M.,
Sharp,L.G., Spollen,W.G., Ries,J., Guillen,A., Khambati,A.,
Topinka,C., Davis,G.E., Schachtman,D., Wu,Y. and Nguyen,H.T.
NSF Grant DBI-0211842: Functional Genomics of Root Growth and Root
Signaling Under Drought
Unpublished (2003)
Contact: Hans Bohnert
University of Illinois, Urbana-Champaign
1201 West Gregory Drive, Urbana, IL 61801, USA
Tel: 217-265-5475
Fax: 217-333-5574
Email: bohnert@life.uiuc.edu
POLYA=Yes.
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## FEATURES

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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:4577"
/clone_lib="zmrws05"
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/note="Samples were collected in Robert E. Sharp's lab (University of Missouri-Columbia) to construct three normalized cDNA libraries. Dark-grown maize seedlings with primary roots 12-20 mm in length were transplanted to high (~0.03 MPa) or low water potential (-1.6 MPa) vermiculite, and harvested at 5 h and 48 h after transplanting. About 1,000 roots were used for each of the low water potential libraries (zmrws05 and zmrws48) while 500 roots were combined from each of the two time points at high water potential (zmrws00). Each root was divided into 4 segments (distances are from the junction of the root apex and root cap): segment 1, 0-3 mm plus the root cap; segment 2, 3-7 mm; segment 3, 7-12 mm; segment 4, 12-20 mm. (For details of conditions see (1) with nutrient modifications as in (2)). The three normalized cDNA libraries were constructed in the lab of Hans Bohnert (University of Illinois-UC). Total RNA was extracted by the 'hot Phenol' method (Plant Molecular Biology manual. D5: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present



Db 114 ACTACTTGGGTTTGTGTAATTATTATGACAGCTTGGTATTGTAATTCAGCTGGGCTACC 55  
Qy 300 CTGGACATTGTTATGTATTATAAATGCTTTGC 332  
Db |||||||||||||||||||||||||||||||  
54 CTGGACATTGTTATGTATTATAAAGCTTTGC 22

Search completed: March 8, 2006, 05:42:24  
Job time : 2670.19 secs



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1	329	100.0	332	7	US-10-603-524A-1	Sequence 1, Appli
2	329	100.0	1236	9	US-10-425-114-13754	Sequence 13754, A
3	329	100.0	7545	9	US-10-508-166-10	Sequence 10, Appli
4	329	100.0	11643	9	US-10-508-166-11	Sequence 11, Appli
5	327.4	99.5	12067	7	US-10-425-114-32117	Sequence 32117, A
6	327.4	99.5	1271	7	US-10-425-114-5509	Sequence 5509, Ap
7	316.4	96.2	725	7	US-10-425-114-5169	Sequence 5169, Ap
8	315	95.7	526	7	US-10-425-114-5111	Sequence 5111, Ap
9	301.4	91.6	1294	8	US-10-739-930-3058	Sequence 3058, Ap
10	294	89.4	1057	7	US-10-425-114-1933	Sequence 1933, Ap
11	286	86.9	818	7	US-10-425-114-35874	Sequence 35874, A
12	278.4	84.6	458	7	US-10-425-114-5192	Sequence 5192, Ap
13	278.4	84.6	1216	7	US-10-425-114-25328	Sequence 25328, A
14	265.6	80.7	1391	8	US-10-425-115-153098	Sequence 153098, A
15	235.4	71.6	594	7	US-10-425-114-36047	Sequence 36047, A
16	232.6	70.7	1234	7	US-10-425-114-24766	Sequence 24766, A
17	232.6	70.7	1278	7	US-10-425-114-27672	Sequence 27672, A
18	204	62.0	1057	7	US-10-425-114-2886	Sequence 2886, Ap
19	187.8	57.1	325	8	US-10-425-115-65927	Sequence 65927, A
20	183.2	55.7	338	8	US-10-425-115-142679	Sequence 142679, A
21	169.4	51.5	611	8	US-10-425-115-108780	Sequence 108780, A
22	142	43.2	1203	8	US-10-425-115-156913	Sequence 156913, A
23	132.4	40.2	4708	8	US-10-425-115-119522	Sequence 119522, A

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Db	181	GTGTTGCTGCTGTGTAGGCTTTGGTAGCATAGGCCCTTATTGCTTCTCGGATGTTGTGT	240
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RESIT.T. 2

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US-10-425-114-13754
; Sequence 13754, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 13754
; LENGTH: 1236
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-039-B10_FLI
US-10-425-114-13754

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### RESULT 3

US-10-508-166-10  
; Sequence 10, Application US/10508166  
; Publication No. US20050223430A1

:	GENERAL INFORMATION:				
:	APPLICANT: PLANT RESEARCH INTERNATIONAL BV				
:	APPLICANT: BAKKER, Hendrikus A.C.				
:	APPLICANT: FLORACK, Dionisius E.A.				
:	APPLICANT: BOSCH, Hendrik J.				
:	TITLE OF INVENTION: Gntiii expression in plants				
:	FILE REFERENCE: 62862A - P033313WO				
:	CURRENT APPLICATION NUMBER: US/10/508,166				
:	CURRENT FILING DATE: 2004-09-17				
:	PRIOR APPLICATION NUMBER: US-60/365,769				
:	PRIOR FILING DATE: 2002-03-19				
:	PRIOR APPLICATION NUMBER: US-60/368,047				
:	PRIOR FILING DATE: 2002-03-26				
:	NUMBER OF SEQ ID NOS: 27				
:	SOFTWARE: PatentIn version 3.2				
:	SEQ ID NO 10				
:	LENGTH: 7545				
:	TYPE: DNA				
:	ORGANISM: Artificial Sequence				
:	FEATURE:				
:	OTHER INFORMATION: Synthetic				
:	US-10-508-166-10				
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	Best Local Similarity	99.1%;	Pred.No. 4.7e-89;		
	Matches 329;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
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Dd	3273	GGTCGCAGCGTGTGCGTGTCGCCGTGTCACGTCTTGGCCGCGCCGGCCCTTGGCGCGCGCATC	3332		
Qy	61	AGAANCCTTGCGTTGCGGTGTGTGTCCTTCTGGTTTGCCTTAATTTTACCAGTTTTGTTT	120		
Dd	3333	AGAAGCGTTTGGCTTGGCGTGTGTGTCCTTCTGGTTTGCCTTAATTTTACCAGTTTTGTTT	3392		
Qy	121	CAAGGTGGATCGCGTGGTCAGGCCCGTGTGCTTTAAANACCACCGGCACCTGGCAGTGA	180		
Dd	3393	CAAGGTGGATCGCGTGGTCAGGCCCGTGTGCTTTAAAGACCCACCGGCACCTGGCAGTGA	3452		
Qy	181	GTGCTGCTGCTTGCTGTAGGCTTTGGTACGTATGCGGCTTTATTGCTTCTGGATGTTGTGT	240		
Dd	3453	GTGCTGCTGCTTGCTGTAGGCTTTGGTACGTATGCGGCTTTATTGCTTCTGGATGTTGTGT	3512		
Qy	241	ACTACTTGGGTTTGGTTGAATTATTATGANCAGTTGGGTATTGTAAATTCAGCTGGGCTACC	300		
Dd	3513	ACTACTTGGGTTTGGTTGAATTATTATGACGAGTTGGGTATTGTAAATTCAGCTGGGCTACC	3572		
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## RESIN.T 4

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US-10-508-166-11
; Sequence 11, Application US/10508166
; Publication No. US20050223430A1
; GENERAL INFORMATION:
; APPLICANT: PLANT RESEARCH INTERNATIONAL BV
; APPLICANT: BAKKER, Hendrikus A.C.
; APPLICANT: FLORACK, Dionisius E.A.
; APPLICANT: BOSCH, Hendrik J.
; TITLE OF INVENTION: GntII expression in plants
; FILE REFERENCE: 62862A - P0333131WO
; CURRENT APPLICATION NUMBER: US/10/508,166
; CURRENT FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: US-60/365,769
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US-60/369,047
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 11643

```







Db 236 AGAAGCGTGGTGGCGGTGTGCTCTGGTTGCTTAATTTACCAAGTTGTTT 295  
Qy 121 CAAGTGATGCGTGGTCAAGGCCCGGTGTGCTTTAAANACCACCGGACCTGGCAGTGA 180  
Db 296 CAAGTGATGCGTGGTCAAGGTCCGTGTGCTTTAAAGACCCACCGGACCTGGCAGTGA 355  
Qy 181 GTGTGCTGCTGTGTAGGCTTTGGTAGCTATGGCTTTATTTGCTTCTGGATGTTGTT 240  
Db 356 GTGTGCTGCTGTGTAGGCTTTGGTAGCTATGGCTTTATTTGCTTCTGGATGTTGTT 415  
Qy 241 ACTACTTGGGTTTGTGTAATTATTATGANCAGTTGCGTATTGT 283  
Db 416 ACTACTTGGGTTTGTGTAATTATTATGAGCAGTTGCGTATTGT 458

## RESULT 13

US-10-425-114-25328  
; Sequence 25328, Application US/10425114  
; Publication No. US20040034888A1

GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 25328

; LENGTH: 1216

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3732-051-F3\_FLI

US-10-425-114-25328

Query Match 84.6%; Score 278.4; DB 7; Length 1216;  
Best Local Similarity 98.6%; Pred. No. 5, 2e-74;  
Matches 279; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGTCCAGCGTGGCTGCGTCCGTCTGCTTCTGCGCGCGGCGCTTTGGCGCGGATC 60  
Db 934 GGTCCAGCGTGGCTGCGTCCGTCTGCTTCTGCGCGCGGCGCTTTGGCGCGGATC 993

Qy 61 AGAAGCGTGGTGGCGGTGTGCTCTGGTTGCTTTAATTTACCAAGTTGTTT 120  
Db 994 AGAAGCGTGGTGGCGGTGTGCTCTGGTTGCTTTAATTTACCAAGTTGTTT 1053

Qy 121 CAAGTGATGCGTGGTCAAGGCCCGGTGTGCTTTAAANACCACCGGACCTGGCAGTGA 180  
Db 1054 CAAGTGATGCGTGGTCAAGTCCGTGTGCTTTAAAGACCCACCGGACCTGGCAGTGA 1113

Qy 181 GTGTGCTGCTGTGTAGGCTTTGGTAGCTATGGCTTTATTTGCTTCTGGATGTTGTT 240  
Db 1114 GTGTGCTGCTGTGTAGGCTTTGGTAGCTATGGCTTTATTTGCTTCTGGATGTTGTT 1173

Qy 241 ACTACTTGGGTTTGTGTAATTATTATGANCAGTTGCGTATTGT 283

Db 1174 ACTACTTGGGTTTGTGTAATTATTATGAGCAGTTGCGTATTGT 1216

## RESULT 14

US-10-425-115-153098

; Sequence 153098, Application US/10425115

; Publication No. US20040214272A1

GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 153098  
; LENGTH: 1391  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(1391)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_71207C.1  
US-10-425-115-153098

Query Match 80.7%; Score 265.6; DB 8; Length 1391;  
Best Local Similarity 93.1%; Pred. No. 4, 4e-70;  
Matches 325; Conservative 0; Mismatches 7; Indels 17; Gaps 4;

Qy 1 GGTCCAGCGTGGCTGCGTCCGTCTGCTGCTGCTTCTGCGCGCGGCGCC---TTGGGCGCGCG 57  
Db 1004 GGTCCAGCGTGGCTGCGTCCGTCTGCTGCTGCTTCTGCGCGCGGCGCTTATTTGGGCGCGCG 1063

Qy 58 ATCAGAACGTTGGCTTG-GCGTGTGTGCTTCTGCTTCTGCTTCTTAAATTTACCAA-GTT 115  
Db 1064 ATCAGAACGTTGGCTTGCGTGTGTGCTTCTGCTTCTGCTTCTTAAATTTACCAAATGTT 1123

Qy 116 TGTTCAGGTGGATCGCGTGGTCAAGCCCGTGTCTTTAAANACCACCGGACCTGGC 175  
Db 1124 TGTTCAGGTGGATCGCGTGGTCAAGTCCGTGTCTTTAAAGACCCACCGGCGAGTGGC 1183

Qy 176 AGTCAGTGTGCTGCTGTGTAGGCTTTGGTAGCTGTGGCTTTATTTGCT- 226  
Db 1184 AGTCAGTGTGCTGCTGTGTAGGCTTTGGTAGCTGTGGCTTTATTTGCTTCCAAATGCTTGC 1243

Qy 227 ---TCTGATGTTGTACTACTTGGGTTTCTTGAATTTATGANCAGTTGCGTATTGT 283  
Db 1244 GGGTCTGAGTGTGTGTACTACTTGGGTTTCTCGAATTTATGAGCAGTTGCGTATTGT 1303

Qy 284 AATTGAGTGGGCTACCTGGACATTTATGATTAATAAATGCTTTC 332

Db 1304 AATTGAGTGGGCTACCTGGACATTTATGATTAATAAATGCTTTC 1352

## RESULT 15

US-10-425-114-36047

; Sequence 36047, Application US/10425114

; Publication No. US20040034888A1

GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 36047

; LENGTH: 594

; TYPE: DNA

; ORGANISM: Zea mays subsp. mexicana

; FEATURE:

; OTHER INFORMATION: Clone ID: UC-ZMROTBOSINTE033G04\_FLI

US-10-425-114-36047



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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	183	55.6	1676	9	US-11-096-568A-24715	Sequence 24715, A	
2	36	10.9	567	6	US-09-925-065A-409218	Sequence 409218, A	
3	35.8	10.9	582	6	US-09-925-065A-815284	Sequence 815284, A	
4	35.8	10.9	583	6	US-09-925-065A-855422	Sequence 855422, A	
5	35.6	10.8	560	6	US-09-925-065A-626220	Sequence 626220, A	
6	35.4	10.8	568	6	US-09-925-065A-249647	Sequence 249647, A	
7	35.4	10.8	568	6	US-09-925-065A-249651	Sequence 249651, A	
8	35.4	10.8	6499	12	US-11-011-332A-91	Sequence 91, Appl	
9	34.8	10.6	677	6	US-09-925-065A-917185	Sequence 917185, A	
10	34.8	10.6	677	6	US-09-925-065A-917186	Sequence 917186, A	
11	34.8	10.6	3737	8	US-10-276-233A-7	Sequence 7, Appl	
12	34.8	10.6	175100	12	US-11-121-086-21	Sequence 21, Appl	
13	34.6	10.5	196716	9	US-11-114-798-53	Sequence 53, Appl	
14	33.8	10.3	63693	8	US-10-995-561-13269	Sequence 13269, A	
15	33.2	10.1	512	6	US-09-925-065A-243873	Sequence 243873, A	
16	33.2	10.1	546	6	US-09-925-065A-449515	Sequence 449515, A	
17	33.2	10.1	612	6	US-09-925-065A-665533	Sequence 665533, A	
18	33.2	10.1	630	6	US-09-925-065A-750364	Sequence 750364, A	
19	33.2	10.1	630	6	US-09-925-065A-750365	Sequence 750365, A	
20	33.2	10.1	735	6	US-09-925-065A-92022	Sequence 92022, A	

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RESULT 2
US-09-925-065A-409218/c
; Sequence 409218, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 409218
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-409218

Query Match      10.9%; Score 36; DB 6; Length 567;
Best Local Similarity 48.0%; Pred. No. 1.5;
Matches 96; Conservative 1; Mismatches 103; Indels 0; Gaps 0;

94 TTTGCTTTAATTTTACCAAGTTGTTTCAAGTGGATCGGTGTCACAGGCCCGTGTGCT 153
239 TATGGTAATAGATTTTAAAGATGTTTAAAGAGGAGCTCAATGGTTAAAGTCAGCTTAA 180
154 TTAANACCACCGGCACGTGGCAGTGAGTGTGCTGTGTAGCTTTGGTACGTATG 213
179 TTAAGCCAGCATCAAGATGATGTGTTGTGTGTGTGTGTGTATTTAAAG 120
214 GCCTTTATTTGCTTCGGAATGTTGTACTACTTGGGTTTGTGAATATTATGANCAGT 273
119 GCCTTCATGTTGTGTTGTTTCTCTCTCTAGGACCTTCTCTCTTTTGTGACAAA 60
274 TCGGTATTTCTAATTCAGCTG 293
59 AATGTTTTTCTTCTCAGTTG 40

RESULT 3
US-09-925-065A-815284
; Sequence 815284, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 815284
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-815284

Query Match      10.9%; Score 35.8; DB 6; Length 582;
Best Local Similarity 49.7%; Pred. No. 1.7;
Matches 88; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

105 TTTACCAAGTTTGTTCAGGTGGATCGGTGTCACAGGCCCGTGTGCTTTAAANACCCA 164
185 TTTAAAAAGATTTTAAAGGAGCTCAATGGTTAAAGTCAGCTTAATTTAAAGCTAACA 244
165 CCGGCACCTGGCAGTGAGTGTGCTGTGTAGCTTTGGTACGTATATGGCTTTATTG 224
245 TCCAAGATGTGTGTGTATGTGTCATATGTGTGTGTATTATTAAAGCCTTTCAAG 304
225 CTCTCGAATGTTGTGTACTACTTGGGTTTGTGAATATTATTATGANCAGTTGCGTATT 281
305 TTTTGTCTTTTGTCTTCTCTAGGACCTTCTCTCTTTTGTGACCAAAAGTTTATT 361

RESULT 4
US-09-925-065A-855422
; Sequence 855422, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 855422
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-855422

Query Match      10.9%; Score 35.8; DB 6; Length 583;
Best Local Similarity 49.7%; Pred. No. 1.7;
Matches 88; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

105 TTTACCAAGTTTGTTCAGGTGGATCGGTGTCACAGGCCCGTGTGCTTTAAANACCCA 164
186 TTTAAAAAGATTTTAAAGGAGCTCAATGGTTAAAGTCAGCTTAATTTAAAGCTAACA 245
165 CCGGCACCTGGCAGTGAGTGTGCTGTGTAGCTTTGGTACGTATATGGCTTTATTG 224
246 TCCAAGATGTGTGTGTATGTGTCATATGTGTGTGTATTATTAAAGCCTTTCAAG 305
225 CTCTCGAATGTTGTGTACTACTTGGGTTTGTGAATATTATTATGANCAGTTGCGTATT 281
306 TTTTGTCTTTTGTCTTCTCTAGGACCTTCTCTCTTTTGTGACCAAAAGTTTATT 362

RESULT 5
US-09-925-065A-626220
; Sequence 626220, Application US/09925065A
; Publication No. US20040181048A1
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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 626220
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-626220

Query Match 10.8%; Score 35.6; DB 6; Length 560;
Best Local Similarity 57.9%; Fred. No. 2;
Matches 62; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 212 TGGGCTTTATTGCTTCTCGGATGTTGTGTACTACTTTGGTTGTTGTAATTATTGACCA 271
Db 191 TGGAAATTATTATCTTTTGGATGCGTATTTAAATTTGGTTGCTAGTATTTTGTGAGTA 250

Qy 272 GTTCGCGATTGTGAATTCAGCTGGGCTACCTCGGACATTGTTAATGATT 318
Db 251 ATTTTGTGCTGTTATTTATCTTCGAGTATCATCTCTGACTGTTTTTTTT 297

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```

RESULT 6
US-09-925-065A-249647
; Sequence 249647, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827,135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 249647
; LENGTH: 568
; .TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-249647

Query Match      10.8%; Score 35.4; DB 6; Length 568;
Best Local Similarity 57.3%; Pred.No.2.3;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

209 GTATGGCGCTTTATTGCTTCTCGAATGTTGTGTACTTGGTGGTTGTTGTAATTATGA 268

```

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Db      383 GTTTTTCTTTGTTTTGTGTTTTGTGTTTGTTTTGTGTTTCAATTTA 442
Qy      269 NCAGTTGGTATTGAATTCACGTGGCGGTACCTGCACATTTGTTATGTATT 318
        ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      443 GCAATGCTTACTTTATGACATAAGAATGTTTCAGGCTAAATTTTGTGTA 492

RESULT 7
US-09-925-065A-249651
; Sequence 249651, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 249651
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-249651

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Query Match	10.8%;	Score 35.4;	DB 6;	Length 568;
Best Local Similarity	57.3%;	Pred. No. 2.3;		
Matches 63;	Conservative 0;	Mismatches 47;	Indels 0;	Gaps 0

  

Qy	209	GTATGGGCTTTATTTGCTTCCTCGAATGTTGTGTACTACTTGGGTTTGTGAATATTATTGA	268
Db	383	GTTTTTCTTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTCATTTTA	442
Qy	269	NCACTTGGGTATTTGTAATTGCTGGGGCTACCTGGACATTTGTTATGATT	318
Db	443	KCATGTGCTTACTTTATGACATAGATGTTTCAGGCTAAATTTGTGTAAT	492

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RESULT 8
US-11-011-332A-91
; Sequence 91, Application US/11011332A
; Publication No. US20060024684A1
; GENERAL INFORMATION:
; APPLICANT: Foekens, John
; APPLICANT: Harbeck, Nadia
; APPLICANT: Koenig, Thomas
; APPLICANT: Maier, Sabine
; APPLICANT: Martens, John
; APPLICANT: Model, Fabian
; APPLICANT: Nimmrich, Inko
; APPLICANT: Rujan, Ramas
; APPLICANT: Schmitt, Manfred
; APPLICANT: Lesche, Ralf
; APPLICANT: Dietrich, Dima
; APPLICANT: Mueller, Volkmar
; APPLICANT: Kluth, Antje
; APPLICANT: Schwobe, Ina
; APPLICANT: Hartmann, Oliver
; APPLICANT: Adorjan, Peter
; TITLE OF INVENTION: PROGNOSTIC MARKER
; DATE OF INVENTION: BREAST CELL PRO
; FILE REFERENCE: 47675-99

```

```

Query Match      10.8%; Score 35.4; DB 6; Length 568;
Best Local Similarity 57.3%; Pred. No. 2.3;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy      209 GTATGGGCTTTATTGCTTCTCGAATGTTGTACTACTTGGTGGTGGTAAATTATGA 268

```

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; CURRENT APPLICATION NUMBER: US/11/011.332A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 10/517,741
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: PCT/EP2004/014170
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: EP 03090432.0
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: EP 04090041.7
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: EP 04090380.9
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: EP 04090127.4
; PRIOR FILING DATE: 2004-04-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 91
; LENGTH: 6499
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-11-011-332A-91

Query Match      10.8%; Score 35.4; DB 12; Length 6499;
Best Local Similarity 46.8%; Pred. No. 4.6;
Matches 108; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

Qy      88  TTCTGTTTGGCTTTAAATTTACCAAGTTTGTTCACAGTGGATCGCGGTCAAGGCCCG 147
Db      88  TTTTGTGGATGGTTGTAATTTTGTGGAGTGGTTATAGGTTGATAGGTTGATTTTGTG 3663

Qy      148  TTGCTTTAAANACCCACCGCAGTGGCAGTGGTGTCTGTGTAGGCTTTGGTA 207
Db      148  TATGAGGTAAAGTAAAGATTAAATGATAGGTTATGATAGAGGTGTGATTTTGTG 3723

Qy      208  CGTATGGCTTTATTTGCTTCGATGTGTACTACTGCTGGTTGTTGTAATTAATG 267
Db      208  TTTTGTGGATGGTTGTAATTTTGTGGAGTGGTTATAGGTTGATAGGTTGATTTTGTG 3783

Qy      3724  TTAATAATTTTGATTTATTTATGTAAGTTTGTGTTTAAATTTGTTTTTGGAGTATTAATG 3783
Db      3724  TTTTGTGGATGGTTGTAATTTTGTGGAGTGGTTATAGGTTGATAGGTTGATTTTGTG 3783

Qy      268  ANCAGTTCGTATTTGTAATTCAGCTGGGCTACCTCGACATGTTATGATT 318
Db      268  TTTTGTGGATGGTTGTAATTTTGTGGAGTGGTTATAGGTTGATAGGTTGATTTTGTG 3834
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```
RESULT 9
US-09-925-065A-917185
; Sequence 917185, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
```

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; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 917185
; LENGTH: 677
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-917185
```

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Query Match      10.6%; Score 34.8; DB 6; Length 677;
Best Local Similarity 60.0%; Pred. No. 3.5;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy      17  TGTCGCTGCTACGTTCTGGCGCGCGGCTTGGCGGCGGATCAGAACGTTGCGTTGG 76
Db      17  TGTCGCTGCTACGTTCTGGCGCGCGGCTTGGCGGCGGATCAGAACGTTGCGTTGG 76

Qy      479  TGTGAGCTGCTCTTCAGGACAGCTGGGCCAAGGATGCTGGAGCTCAGACCTTCAGTGG 538
Db      479  TGTGAGCTGCTCTTCAGGACAGCTGGGCCAAGGATGCTGGAGCTCAGACCTTCAGTGG 538

Qy      77  CGTGTGTGTGCTTCTGCTGTTTCTTTAAATTTTACCA 111
Db      77  CGTGTGTGTGCTTCTGCTGTTTCTTTAAATTTTACCA 111

Qy      539  GGTCTGTGTCTCTGCTGCTCAACGTCATTTCTTCCCA 573
Db      539  GGTCTGTGTCTCTGCTGCTCAACGTCATTTCTTCCCA 573
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RESULT 10
US-09-925-065A-917186
; Sequence 917186, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 917186
; LENGTH: 677
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-917186
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Query Match      10.6%; Score 34.8; DB 6; Length 677;
Best Local Similarity 60.0%; Pred. No. 3.5;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy      17  TGTCGCTGCTACGTTCTGGCGCGCGGCTTGGCGGCGGATCAGAACGTTGCGTTGG 76
Db      17  TGTCGCTGCTACGTTCTGGCGCGCGGCTTGGCGGCGGATCAGAACGTTGCGTTGG 76

Qy      479  TGTGAGCTGCTCTTCAGGACAGCTGGGCCAAGGATGCTGGAGCTCAGACCTTCAGTGG 538
Db      479  TGTGAGCTGCTCTTCAGGACAGCTGGGCCAAGGATGCTGGAGCTCAGACCTTCAGTGG 538

Qy      77  CGTGTGTGTGCTTCTGCTGTTTCTTTAAATTTTACCA 111
Db      77  CGTGTGTGTGCTTCTGCTGTTTCTTTAAATTTTACCA 111

Qy      539  GGTCTGTGTCTCTGCTGCTCAACGTCATTTCTTCCCA 573
Db      539  GGTCTGTGTCTCTGCTGCTCAACGTCATTTCTTCCCA 573
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RESULT 11
US-10-276-233A-7
; Sequence 7, Application US/10276233A
; Publication No. US20050260572A1
; GENERAL INFORMATION:
; APPLICANT: DNA Chip Research Inc.
; APPLICANT: Hitachi Software Engineering Co., Ltd.
; TITLE OF INVENTION: A method of predicting cancer condition
; FILE REFERENCE: PH-1533-PCT
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, CURRENT APPLICATION NUMBER: US/10/276,233A
,
, CURRENT FILING DATE: 2002-11-14
,
, PRIOR APPLICATION NUMBER: JP 2001-73063
,
, PRIOR FILING DATE: 2001-03-14
,
, PRIOR APPLICATION NUMBER: JP 2001-108503
,
, PRIOR FILING DATE: 2001-04-06
,
, PRIOR APPLICATION NUMBER: JP 2001-234807
,
, PRIOR FILING DATE: 2001-08-02
,
, NUMBER OF SEQ ID NOS: 27
,
, SOFTWARE: PatentIn Ver. 3.2
,
, SEQ ID NO 7
,
, LENGTH: 33737
,
, TYPE: DNA
,
, ORGANISM: Homo sapiens
US-10-276-233A-7

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	Query Match	10.6%	Score 34.8;	DB 8;	Length 33737;
	Best Local Similarity	60.0%;	Pred. No. 11;		
	Matches 57;	Conservative 0;	Mismatches 38;	Indels 0;	Gaps 0;
Qy	17	TGTCGTGTGACGTTCTGCGCGCGCGGCTTGGGCGCGCATCAGAACGTCGTGGTGG	76		
Db	26246	TGTGAGTGTCCTCTCAGGACAGCTGGCGCAAGATGCTGGAGCTCAGACCTTCGAGTGG			
Qy	77	CGTGTGTGTGCTCTCGTTTGCTTTAATTTTACCA	111		
Db	26306	GGTCTGTGTCCTGTGTGTCAACGTCATCTTCTCCA	26340		

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RESULT 12
US-11-121-086-21
; Sequence 21, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 175100
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-21

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		Best Local Similarity	60.0%;	Pred. No. 18;			
		Matches	57;	Conservative	0;	Mismatches	38;
						Indels	0;
						Gaps	0;
Qy	17	TGTCCTGTGTACCTTCTGGCCGCCGCCTTTGGCGCCGCATCAGAACNCGTTGGCTTG	76				
Db	79714	TGTGAGTGCTCTTTCAGCACAGCTGGGCCAAGTAGCTGGAGCTCAGACCTTGCAGTGG	79773				
Qy	77	CGTGTGTGTGCTTCTCGTTTTGCTTTAAATTTTACC	111				
Db	79774	GGTCTGTGTCCTTGTGTGCAAGCTATTCTTCCCA	79808				

RESULT 13  
US-11-114-798-53  
; Sequence 53, Application US/11114798  
; Publication No. US20060035246A1  
; GENERAL INFORMATION:  
; APPLICANT: WU, RINA  
; APPLICANT: MARQUEZ, ABBEY  
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND  
; TITLE OF INVENTION: COMPOSITIONS  
; FILE REFERENCE: 0618.011.0004

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? CURRENT APPLICATION NUMBER: US/11/114,798
?
? CURRENT FILING DATE: 2005-04-26
?
? PRIOR APPLICATION NUMBER: 10/173,525
?
? PRIOR FILING DATE: 2002-06-17
?
? PRIOR APPLICATION NUMBER: 09/952,851
?
? PRIOR FILING DATE: 2001-09-14
?
? NUMBER OF SEQ ID NOS: 58
?
? SOFTWARE: PatentIn Ver. 3.3
?
? SEQ ID NO 53
?
? LENGTH: 196716
?
? TYPE: DNA
?
? ORGANISM: Artificial Sequence
?
? FEATURE:
?
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
?
? OTHER INFORMATION: nucleotide sequence
?
? US-11-114-798-53

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	Query Match	10.5%;	Score 34.6;	DB 9;	Length 196716;
	Best Local Similarity	57.5%;	Pred. No. 22;		
	Matches 61;	Conservative 0;	Mismatches 45;	Indels 0;	Gaps 0;
Qy	216	CTTTATTGCTTCTGGATGTTGTGTACTACTTGGGTTTTGTTGAATTATATGANCAGTTG	275		
Db	31777	CATAAATAGGTGTAGATTTTGTCAAATGCTTTTTTTCATCAATTAATAATGATCATATG	31836		
Qy	276	CGTATTGTAATTCAGCTGGGCTACCTGGACATTTGTTATGTTAAT	321		
Db	31837	ATCCCTTCTAATTCAGCTTTGTCATATGGTGATCAATCATGTTGAT	31882		

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RESULT 14
; US-10-995-561-13269
; Sequence 13269, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13269
; LENGTH: 63693
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-995-561-13269

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Query Match	10.3%;	Score 33.8;	DB 8;	Length 63693;	
Best Local Similarity	48.6%;	Pred. No. 26;			
Matches 118;	Conservative	0;	Mismatches 124;	Indels 1;	Gaps 1;
Qy	84	GTGCTTCGTGTTTGGCTTTAAATTTTACCAAGTTTGTTC	CAAGTGGATCGCGTGTCAAGG	143	
Db	48715	GAGATTCGTATGTTGTATCTTTATTCTCATTTAGTTC	CAAGAACTTCCTGATTC-TGC	48773	
Qy	144	CCCGTGTGCTTTAAANACCCACCGGCATCGCAGTGAGTGT	TGCTGCTTGTGTAGGCTTTT	203	
Db	48774	CATAATTTCAATTTTACCACCAAAAGTCATTCAGGAGCA	TGTTGTGATTTCCCATGTAAT	48833	
Qy	204	GGTAGCTATGGSCTTTATTTCCTTCGGATGTTGTGTACT	ACTTGGGTTGCTGCAATAT	263	
Db	48834	TGTACGGTTTTGAGTATTTTCTTAGCTCTTGACTGTAT	TATTCATTGTGCTGTGCTGAG	48893	
Qy	264	TATGANCACTTCGGTATTTGTAAATTCAGCTGGGCTAC	CTGGACATTTGTTATGTAATAA	323	
Db	48894	AGTGTGTTTGGTATGATTTTGGTCTTTGGGCACACT	GTCTGAAGATGTTTTATGTCCAATT	48953	
Qy	324	ATG 326			
Db	48954	ATG 48956			

Search completed: March 8, 2006, 06:10:10  
Job time : 887.156 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 23:00:44 ; Search time 139.621 Seconds  
(without alignments)  
4226.797 Million cell updates/sec

Title: US-10-603-524A-1

Perfect score: 329

Sequence: 1 ggtcagcgtgtgctgtc.....tgtattaataaagtgttgc 332

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/prodata/1/ina/1 COMB.seq:\*
- 2: /cgn2\_6/prodata/1/ina/5 COMB.seq:\*
- 3: /cgn2\_6/prodata/1/ina/6A COMB.seq:\*
- 4: /cgn2\_6/prodata/1/ina/6B COMB.seq:\*
- 5: /cgn2\_6/prodata/1/ina/H COMB.seq:\*
- 6: /cgn2\_6/prodata/1/ina/PCTUS COMB.seq:\*
- 7: /cgn2\_6/prodata/1/ina/PP COMB.seq:\*
- 8: /cgn2\_6/prodata/1/ina/RE COMB.seq:\*
- 9: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	27.7	1333	2	US-08-288-630-1
2	84.8	25.8	758	2	US-08-288-630-1
3	76.6	23.3	291	3	US-09-313-294A-6335
4	37.6	11.4	67643	3	US-09-949-016-14760
5	35.4	10.8	17146	3	US-09-949-016-16774
6	34.8	10.6	100990	3	US-09-409-800B-2
7	34.2	10.4	126176	3	US-09-949-016-16137
8	34.2	10.4	451924	3	US-09-949-016-16138
9	34.2	10.4	451924	3	US-09-949-016-12896
10	34.2	10.4	451925	3	US-09-949-016-17305
11	33.8	10.3	924	3	US-09-248-796A-1471
12	33.8	10.3	55195	3	US-09-949-016-15854
13	33.2	10.1	300598	3	US-09-949-016-11868
14	33.2	10.1	308362	3	US-09-949-016-17119
15	33.2	10.1	4403765	3	US-09-103-840A-2
16	33.2	10.1	4411529	3	US-09-103-840A-1
17	33	10.0	70000	3	US-09-851-896-3
18	33	10.0	76399	3	US-09-949-016-16819
19	33	10.0	146307	3	US-09-949-016-14881
20	33	10.0	146307	3	US-09-949-016-14882
21	33	10.0	146307	3	US-09-949-016-14883
22	33	10.0	146307	3	US-09-949-016-14884
23	33	10.0	146307	3	US-09-949-016-14885
24	33	10.0	146307	3	US-09-949-016-14886

C 25	33	10.0	146307	3	US-09-949-016-14887
C 26	33	10.0	146307	3	US-09-949-016-14888
C 27	33	10.0	148405	3	US-09-949-016-11747
C 28	33	10.0	148405	3	US-09-949-016-12835
C 29	33	10.0	148405	3	US-09-949-016-12836
C 30	33	10.0	148405	3	US-09-949-016-12837
C 31	32.6	9.9	26134	3	US-09-949-016-15285
C 32	32.6	9.9	145812	3	US-09-949-016-15698
C 33	32.6	9.9	767677	3	US-09-949-016-12147
C 34	32.6	9.9	767677	3	US-09-949-016-17361
C 35	32.4	9.8	399	3	US-09-621-976-8976
C 36	32	9.7	13015	3	US-09-639-207-10
C 37	31.6	9.6	288	3	US-09-513-999C-2582
C 38	31.6	9.6	10758	3	US-08-956-171E-221
C 39	31.6	9.6	10758	3	US-08-781-986A-221
C 40	31.6	9.6	26867	3	US-09-949-016-16332
C 41	31.6	9.6	26867	3	US-09-949-016-16333
C 42	31.6	9.6	285986	3	US-09-949-016-12287
C 43	31.6	9.6	288031	3	US-09-949-016-14864
C 44	31.4	9.5	400	3	US-08-956-171E-4132
C 45	31.4	9.5	400	3	US-08-781-986A-4132

#### ALIGNMENTS

RESULT 1  
US-08-288-630-1  
; Sequence 1, Application US/08288630  
; Patent No. 5837848  
; GENERAL INFORMATION:  
; APPLICANT: ELY, SUSAN  
; APPLICANT: EVANS, IAN J  
; APPLICANT: SCHUCH, WOLFGANG W  
; TITLE OF INVENTION: ROOT-SPECIFIC PROMOTER  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: CUSHMAN DABY & CUSHMAN, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/288,630  
; FILING DATE: 10-AUG-1994  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/111,590  
; FILING DATE: 25-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/669,433  
; FILING DATE: 15-MAR-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9006017.9  
; FILING DATE: 16-MAR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 215964/SHE35669USCIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1333 base pairs  
; TYPE: nucleic acid

Sequence 14887, A  
Sequence 14888, A  
Sequence 11747, A  
Sequence 12835, A  
Sequence 12836, A  
Sequence 12837, A  
Sequence 15285, A  
Sequence 15698, A  
Sequence 12147, A  
Sequence 17361, A  
Sequence 8976, Ap  
Sequence 10, Appl  
Sequence 2582, Ap  
Sequence 221, App  
Sequence 221, App  
Sequence 16332, A  
Sequence 16333, A  
Sequence 12287, A  
Sequence 14864, A  
Sequence 4132, Ap  
Sequence 4132, Ap







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; Sequence 16137, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16137
; LENGTH: 126176
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16137

Query Match      10.4%; Score 34.2; DB 3; Length 126176;
Best Local Similarity 57.7%; Pred. No. 6.6;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 215 GCTTATTGCTCTCGGATGTTGTACTACTGCGTTTGTGAATTATTATGANCAGTT 274
DB 121156 GGTGATTATTGTTTTGTGATGCTCTGGATTCCGATTGGTAGTATTTTGTGAAAAATT 121215

QY 275 GCGTATTGTAATTCAGCTGGGCTACTCGACATTCGTTATGATT 318
DB 121216 TTGCATCTGTCTCATCAGGATATGCTCTATAGTTTTTTGTT 121259

RESULT 8
US-09-949-016-16138
; Sequence 16138, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16138
; LENGTH: 126176
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16138

Query Match      10.4%; Score 34.2; DB 3; Length 126176;
Best Local Similarity 57.7%; Pred. No. 6.6;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 215 GCTTATTGCTCTCGGATGTTGTACTACTGCGTTTGTGAATTATTATGANCAGTT 274
DB 121156 GGTGATTATTGTTTTGTGATGCTCTGGATTCCGATTGGTAGTATTTTGTGAAAAATT 121215

QY 275 GCGTATTGTAATTCAGCTGGGCTACTCGACATTCGTTATGATT 318
DB 121216 TTGCATCTGTCTCATCAGGATATGCTCTATAGTTTTTTGTT 121259

RESULT 9
US-09-949-016-12896
; Sequence 12896, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12896
; LENGTH: 451924
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12896

Query Match      10.4%; Score 34.2; DB 3; Length 451924;
Best Local Similarity 57.7%; Pred. No. 13;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 215 GCTTATTGCTCTCGGATGTTGTACTACTGCGTTTGTGAATTATTATGANCAGTT 274
DB 340246 GGTGATTATTGTTTCTGATGACTGTTGCCATTTGGCTGCTAGTATTTTGTAGGATTA 340305

QY 275 GCGTATTGTAATTCAGCTGGGCTACTCGACATTCGTTATGATT 318
DB 340306 TTGTGTTTACATTTCATCAGGATATTTGGCCTATAGTTTCTATT 340349

RESULT 10
US-09-949-016-17305
; Sequence 17305, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17305
; LENGTH: 451925
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17305

Query Match      10.4%; Score 34.2; DB 3; Length 451925;
Best Local Similarity 57.7%; Pred. No. 13;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 215 GCTTATTGCTCTCGGATGTTGTACTACTGCGTTTGTGAATTATTATGANCAGTT 274
DB 340246 GGTGATTATTGTTTCTGATGACTGTTGCCATTTGGCTGCTAGTATTTTGTAGGATTA 340305

QY 275 GCGTATTGTAATTCAGCTGGGCTACTCGACATTCGTTATGATT 318
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Db	44689	GAGATTCTGGTATGTATCTTTATTTCTCATTTCAAGAACTTCTGATTTCTG	44747
Qy	144	CCCGTGTGCTTTAAANACCCACCGCAGTGGCAGTGAGTGTGTGCTGTGTGAGGCTTT	203
Db	44748	CATAATTTTCATTTATTCACCCAAAAGTCATTCAGGAGCATGTGTTTGATTTCCATGTAAT	44807
Qy	204	GGTACGATATGGCGTTTATTTGCTCTCGATGTTGTGTACTACTTGGGTTTGTGTAATTAAT	263
Db	44808	TGTACGGTTTTCAGTTATTTTCTTAGTCTTGACTGTATTTTCATGTGCTGTGGTCTGAG	44867
Qy	264	TATGANCAGTTCGGTATGTGTAATTCAGCTGGGCTACCTGGACATTTGTTATGTAATAATAA	323
Db	44868	AGTGTGTTTGGTATGATTTTGGTTCTTTGGCATTGCTGAAGATGTTTTATGTCCAAT	44927
Qy	324	ATG 326	
Db	44928	ATG 44930	

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RESULT 13
US-09-949-016-11868/c
; Sequence 11868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11868
; LENGTH: 300598
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(300598)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-11868

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Query Match	10.1%;	Score 33.2;	DB 3;	Length 300598;
Best Local Similarity	51.0%;	Pred. No. 23;		
Matches	77: Conservative	0: Mismatches	74: Indels	0: Gaps

Qy	172	TGGCAGTGA	GTGCTGCT	TGTAGCGT	TTGGTACG	TATGCGCT	TTATTGCT	TCGG	231
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Qy	232	ATGTTGTG	TACTTCGG	TTTGTGAA	TATATGANC	AGTGGCGT	TATGTAAT	TCAGC	291
Db	256604	GTGATCAT	AAGAATGC	TTTGTGTA	ATTCACCT	TATAAGAT	TTTTTTCG	CATCTGG	256545
Qy	292	TGGGCTAC	TGGACATT	GTATGATTA	ATAA				322
Db	256544	AACTTCAG	TGTCCAAT	TTTTTGTG	GTGTTTTA				256514

RESULT 14  
US-09-949-016-17119/c  
; Sequence 17119, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

US-09-949-016-17119/c  
; Sequence 17119, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN K

QY 84 GTGCTTCTGGTTTGCTTTAAATTTACCAAGTTTGTTTCAAGGTGGATCGCGTGGTCAAGG 143

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Query Match      10.1%; Score 33.2; DB 3; Length 4403765;
Best Local Similarity 51.0%; Pred No 88;
Matches 77; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY      160 ACCACCGCACGCGAGTGTTCGCTGTGTGAGGCTTTGGTAGCGATGGCGCTTT 219
Db      4402326 ACCCTCGTCAACGCGAGGGAGCGTAGCTTTTGTGTTGATTTCTTCAGTCTGCAGTTC 4402226

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 04:07:00 ; Search time 2337.81 Seconds  
(without alignments)  
5823.847 Million cell updates/sec

Title: US-10-603-524A-2  
Perfect score: 291  
Sequence: 1 agccggcttatgtcgtag.....tgtgagtgcctatatcaaa 291

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_est3:  
4: gb\_hc:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est7:  
9: gb\_gsal:  
10: gb\_gsal2:  
11: gb\_gsal3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	287.8	98.9	692	DN204218	MEST801.D
C 2	285.8	98.2	451	CF626836	zmrws05_0
C 3	285.8	98.2	675	CF627673	zmrws05_0
C 4	284.6	97.8	448	BE639295	946020E02
C 5	282.6	97.1	404	CF061011	QCT16d11.
C 6	281	96.6	437	CF061154	QCT18c03.
C 7	279.8	96.2	313	BM888666	952067R09
C 8	279.8	96.2	313	BM895191	952066H10
C 9	279.8	96.2	599	AI738207	606047B11
C 10	278.2	95.6	628	AW061962	687009G02
C 11	276.8	95.1	290	BQ163609	952077G01
C 12	276.6	95.1	409	BQ163007	952032D09
C 13	276.6	95.1	461	AW519844	660053H10
C 14	270.6	93.0	289	DN217785	MEST800.E
C 15	270.6	93.0	290	DN223333	MEST1144
C 16	270.4	92.9	280	BE186822	946012H04
C 17	267.8	92.0	312	BM888756	952068H02
C 18	266.8	91.7	619	AW191435	687028F09
C 19	265.6	91.3	614	BU079762	946147C04
C 20	264	90.7	329	BM498022	952032D09
C 21	263.8	90.7	295	DR906452	E0808.Zea
C 22	262.8	90.3	424	BI180447	949036H01

23	261.4	89.8	273	3	BM896196	BM896196	952067H02
C 24	260.2	89.4	342	1	AI619189	AI619189	486086F12
C 25	260.2	89.4	468	2	BG840667	BG840667	MEST14-F0
C 26	260.2	89.4	468	2	BG841013	BG841013	MEST14-F0
C 27	260.2	89.4	536	3	BM381193	BM381193	MEST531-C
C 28	260.2	89.4	548	3	BM380521	BM380521	MEST521-B
C 29	260.2	89.4	556	3	BM382000	BM382000	MEST543-B
C 30	260.2	89.4	602	1	AI621840	AI621840	486027B11
C 31	260.2	89.4	625	8	DN229243	DN229243	MEST1014
C 32	260.2	89.4	629	1	AI622731	AI622731	486106A12
C 33	260.2	89.4	644	6	CA402201	CA402201	ELO1N0433
C 34	260.2	89.4	650	8	CA402201	CA402201	ELO1N0433
C 35	260.2	89.4	661	6	CD434515	CD434515	MEST1111
C 36	260.2	89.4	716	8	DN223155	DN223155	ELO1N0330
C 37	260.2	89.4	719	8	DN221819	DN221819	MEST1138
C 38	260.2	89.4	735	9	BZ622915	BZ622915	1981403.G
C 39	260.2	89.4	815	6	CD445358	CD445358	ELO1N0450
C 40	258.8	88.9	595	5	BU572123	BU572123	946168C02
C 41	258.6	88.9	537	3	BM074032	BM074032	MEST79-C0
C 42	258.6	88.9	634	7	CO529353	CO529353	3530.1.19
C 43	258.6	88.9	652	3	BM380681	BM380681	MEST523-D
C 44	258.4	88.8	270	3	BM896245	BM896245	952068E09
C 45	258.4	88.8	270	3	BQ035196	BQ035196	952077G01

## ALIGNMENTS

RESULT 1  
DN204218/c  
LOCUS DN204218 692 bp mRNA linear EST 28-FEB-2005  
DEFINITION MEST801.D04.T7-1 UGA-ZmSAM-X22 Zea mays cDNA, mRNA sequence.  
ACCESSION DN204218  
VERSION DN204218.1 GI:60337245  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE  
1 (bases 1 to 692)  
Chen,H.D., Zhang,X., Zhou,R.L., Arias L.A.C., Shendelman,J.M., Zazubovite,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J. and Schnable,P.S.  
Expressed Sequence Tags from B73 Maize Shoot Apical Meristems  
Unpublished (2004)  
Contact: Patrick S. Schnable  
Schnable Laboratory  
Iowa State University  
2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA  
Tel: 515-294-0975  
Fax: 515-294-5256  
Email: schnable@iastate.edu.

TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
1..692  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="inbred B73"  
/db\_xref="taxon:4577"  
/tissue\_type="vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4"  
/lab\_host="XLI-Blue"  
/clone\_lib="UGA-ZmSAM-X22"  
/note="Organ: Shoot apex; Vector: Uni-Zap XR; Site 1: EcoRI; Site 2: XhoI; This library was constructed by Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4 from 14-17 day after germination seedlings were quickly dissected into dry ice under a light microscope. Total RNA was isolated using Trizol and mRNA was purified with Dynal Oligo-DT25. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer





QY 121 AATTTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGCCCTCGGTGCCACCTCGTTT 180  
 |||||  
 Db 169 AATTTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGCCCTCGGTGCCACCTCGTTT 110  
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 QY 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTCA 240  
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 Db 109 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTCA 50  
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 QY 241 CTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCTTATATC 289  
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 Db 49 CTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCTTATATC 1

RESULT 4  
 BE639295/c  
 LOCUS BE639295 448 bp mRNA linear EST 30-AUG-2000  
 DEFINITION 946020502.y2 946 - tassels primordium prepared by Schmidt lab Zea  
 mays cDNA, mRNA sequence.

ACCESSION BE639295  
 VERSION BE639295.1 GI:9952607  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 448)

REFERENCE Walbot.V.  
 Maize ESTs from various cDNA libraries sequenced at Stanford

AUTHORS Walbot V.  
 TITLE University  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 946020 row: E column: 02.

FEATURES  
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 1..448  
 Location/Qualifiers  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="OH43"  
 /db\_xref="taxon:4577"  
 /tissue\_type="tassels"  
 /dev\_stage="just after the transition from vegetative to  
 inflorescence development"  
 /lab\_host="XLOLR"  
 /clone\_lib="946 - tassels primordium prepared by Schmidt  
 lab"  
 /note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;  
 Site 2: XhoI; George Chuck dissected immature tassels  
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA  
 library in HybriZAP. Sample insert size range was 350 bp  
 to 3 Kb with a 1 Kb average."

ORIGIN  
 Query Match 97.8%; Score 284.6; DB 2; Length 448;  
 Best Local Similarity 98.6%; Pred. No. 3e-76;  
 Matches 287; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGCGCGCTTATGCGGTAGAAACTAGTAGCTAGTGTGCTGCTGCGAATGACACTAT 60  
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 Db 321 AGCGCGCTTATGCGGTAGAAACTAGTAGCTAGTGTGCTGCTGCGAATGACACTAT 262  
 |||||  
 QY 61 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGAGCTAGTTATGACTGTGTCAGTAA 120  
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 Db 261 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGAGCTGTATGACTGTCTCGTAA 202  
 |||||  
 QY 121 AATTTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGCCCTCGGTGCCACCTCGTTT 180  
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Db 201 AATTTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGCCCTCGGTGCCACCTCGTTT 142  
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 QY 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTCA 240  
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 Db 141 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTCA 82  
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 QY 241 CTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCTTATATCA 291  
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 Db 81 CTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCTTATATCA 31

RESULT 5  
 CF061011/c  
 LOCUS OQT16d11.y9 OQT Zea mays cDNA clone OQT16d11, mRNA sequence.

ACCESSION CF061011  
 VERSION CF061011.1 GI:33101051  
 KEYWORDS EST.

SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 404)

REFERENCE Genoplante.  
 Auteurs  
 TITLE Genoplante, a major partnership french program in plant genomics  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Genoplante

Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplante' (http://www.genoplante.com  
 and http://genoplante-info.infobiogen.fr).

FEATURES  
 Location/Qualifiers  
 1..404

/organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="f333 or f334"  
 /db\_xref="taxon:4577"  
 /clone="OQT16d11"  
 /tissue\_type="seedling minus kernel"  
 /clone\_lib="OQT"

ORIGIN

Query Match 97.1%; Score 282.6; DB 6; Length 404;  
 Best Local Similarity 98.6%; Pred. No. 1.2e-75;  
 Matches 285; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGCGCGCTTATGCGGTAGAAACTAGTAGCTAGTGTGCTGCTGCGAATGACACTAT 60  
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 Db 250 AGCGCGCTTATGCGGTAGAAACTAGTAGCTAGTGTGCTGCTGCGAATGACACTAT 231  
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 QY 61 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGAGCTAGTTATGACTGTGTCAGTAA 120  
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 Db 230 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGAGCTGTATGACTGTGTCAGTAA 171  
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 QY 121 AATTTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGCCCTCGGTGCCACCTCGTTT 180  
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 Db 170 AATTTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGCCCTCGGTGCCACCTCGTTT 111  
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 QY 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTCA 240  
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 Db 110 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTCA 51  
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 QY 241 CTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCTTATATC 289  
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RESULT 6  
 CF061154/c



LOCUS	CF0611154	437 bp	mRNA	linear	EST 21-JUL-2003
DEFINITION	QCT18c03.yg QCT Zea mays cdna clone QCT18c03, mRNA sequence.				
ACCESSION	CF0611154				
VERSION	CF0611154.1 GI:33101194				
KEYWORDS	EST.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 437)				
TITLE	Genoplatte.				
COMMENT	Genoplatte, a major partnership french program in plant genomics				
	Unpublished (2003)				
	Contact: Genoplatte				
	Genoplatte				
	93, rue Henri Rochefort 91025 EVRY CEDEX France				
	Tel: 33 1 69 47 54 00				
	Fax: 33 1 69 47 54 10				
	This sequence has been generated in the framework of the french				
	plant genomics programme 'Genoplatte' ( <a href="http://www.genoplatte.com">http://www.genoplatte.com</a>				
	and <a href="http://genoplatte-info.infobiogen.fr">http://genoplatte-info.infobiogen.fr</a> ).				

**FEATURES**  
**source**

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/cultivar="f333 or f334"
/db_xref="taxon:4577"
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/tissue_type="seedling minus kernel"
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## ORIGIN

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Best Local Similarity	99.3%;	Pred. No. 3.8e-75;		
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Qy 1	AGCGGGTTTTATGTGCGCTAGAAACTAGTAGCTAGTCTGTTGCTGCTGCAATGACACTAT	60		
Db 289	AGCGGGTTTTATGTGCGCTAGAAACTAGTAGCTAGTCTGTTGCTGCTGCAATGACACTAT	230		
Qy 61	GCAATGTGATCTGGAACCTGTTTTCTTTGGGTGCGACGCTAGTATGACTGTCGTCAGTAA	120		
Db 229	GCAATGTGATCTGGAACCTGTTTTCTTTGGGTGCGACGCTGTTATGACTGTTCATCGGTAA	170		
Qy 121	AAATTGGGGGCTCCCGCTATGAGATGCTGCGGGCAAGGCGCTCGGTGTCCACCTCGTTT	180		
Db 169	AAATTGGGGGCTCCCGCTATGAGATGCTGCGGGCAAGGCGCTCGGTGTCCACCTCGTTT	110		
Qy 181	GTGCGGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTGCA	240		
Db 109	GTGCGGGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAACTGTGTGCA	50		
Qy 241	CTTGGCATTTTACCTTTTCCATCGCTGTTTATGTGAGTGGTCTATATC	289		
Db 49	CTTGGCATTTTACCTTTTCCATCGCTGTTTATGTGAGTGGTCTATATC	1		

## RESULT 7

LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
BM888666	952067E09.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea mays CDNA, mRNA sequence.	BM888666	EST.	Zea mays	Rukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	1 (bases 1 to 313)	Walbot.V.

## REFERENCE AUTHORS

Maize ESTs from various cDNA libraries sequenced at Stanford University  
 Unpublished (1999)  
 Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 952067 row: E column: 09.

FEATURES . source

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1. 313
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/cultivar="BMS (Black  

/db_xref="taxon:4577  

/tissue_type="suspension  

/dev_stage="mixed leaf  

phase"
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/clone_lib="952 - BMS"

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rRNA" =  
/note=vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; T:  
library was prepared by George Rudenko using poly (A)  
selected rRNA and Universal Riboclone cDNA Synthesis S  
(Promega). cDNA was synthesized using both random and  
oligo(dT) primers in separate reactions and equipped  
EcoRI adaptors. Library was size-fractionated on agar  
gels (for insert size >400bp) and non-directionally c  
into EcoRI-digested pUC19 vector. Blue/white selection  
carbenicillin-containing plates was used to recover  
positive clones."

## ORIGIN

Query Match	96.2%	Score 279.8;	DB 3;	Length 313;
Best Local Similarity	97.6%;	Pred. No. 8.3e-75;		
Matches 284;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
Qy	1	AGCGCGCTTATGTGCGTAGAACTAGTAGCTAGTGTTCCTGCTCGGAATGACACTAT	60	
Db	293	AGCGCGCTTATGTGCGTAGAACTAGTAGCTAGTGTTCCTGCTCGGAATGACACTAT	234	
Qy	61	GCAATGTGATCTGGAACCTGGTTTCITGGGTGCGACGCTAGTTATGACTGTCGTCAGTAA	120	
Db	233	GCAATGTGATCTGGAACCTGGTTTCITGGGTGCGACGCTAGTTATGACTGTCATCGGTAA	174	
Qy	121	AATTTGGGGGCTCCCGGTATGAGATGCTCGCGGCAAGGCTCGGTGTCGCCACTCGCTTT	180	
Db	173	AATTTGGGGGCTCCCGGTATGAGATGCTCGCGGCAAGGCTCGGTGTCGCCACTCGCTTT	114	
Qy	181	GTGGCGGGGGGCGCTGGAGCCCGGTCTGGTTGGTTGGGAAGCCCTTTAAACTGTTGTCA	240	
Db	113	GTGGCGGGGGGCGCTGGAGCCCGGTCTGGTTGGTTGGGAAGCCCTTTAACTGTTGTCA	54	
Qy	241	CTTGCAATTTTACCTTTTCATCGCTGTTTATTGTGAGTGGTCTCATATCAA	291	
Db	53	CTTGCAATTTTACCTTTTCATCGCTGTTTATTGTGAGTGGTCCGACAGCAA	3	

## RESULT 8

BM895191/C	BM895191	313 bp	linear	EST 11-MAR-2002		
LOCUS	952066H10.y1.952	- BMS tissue from Walbot Lab (reduced rRNA) Zea				
DEFINITION	mays cDNA, mRNA sequence.					
ACCESSION	BM895191					
VERSION	BM895191.1	GI:19350659				
KEYWORDS	EST.					
SOURCE	Zea mays					
ORGANISM	Zea mays					
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.					





**AUTHORS**  
**TITLE** Walbot.V.  
**JOURNAL** Maize ESTs from various cDNA libraries sequenced at Stanford  
**COMMENT** University  
 Unpublished (1999)  
 Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 952032 row: D column: 09.  
**FEATURES**  
 source  
 1. 409  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="BMS (Black Mexican Sweet)"  
 /db\_xref="taxon:4577"  
 /tissue\_type="suspension culture"  
 /dev\_stage="mixed logarithmic and stationary growth phases"  
 /lab\_host="DH108"  
 /clone\_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"  
 /note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

**ORIGIN**

Query Match 95.1%; Score 276.6; DB 3; Length 409;  
 Best Local Similarity 98.6%; Pred. No. 8.4e-74;  
 Matches 279; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 60  
 Db 294 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 235  
 QY 61 GCAATGTGATCTGGAACTGCTGTTCTGGTGGCGAGCTAGTATGACTGTGCTCAGTAA 120  
 Db 234 GCAATGTGATCTGGAACTGCTGTTCTGGTGGCGAGCTGTTGTTATGACTGTGCTCAGTAA 175  
 QY 121 AATTTGGGGGCTCCCGGTATGAGATGCTGCGGGCAAGCCCTCGGTGCCACCTCGTTT 180  
 Db 174 AATTTGGGGGCTCCCGGTATGAGATGCTGCGGGCAAGCCCTCGGTGCCACCTCGTTT 115  
 QY 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGTTGGGTGGGAAGCCCTTTAAACTGTGTGCA 240  
 Db 114 GTGGCGGGGGCGCTGGAGCCCGGTCTGTTGGGTGGGAAGCCCTTTAAACTGTGTGCA 55  
 QY 241 CTTCATTTTACCTTTTCATCGCTGTTTATGAGTGGTCC 283  
 Db 54 CTTCATTTTACCTTTTCATCGCTGTTTATGAGTGGTCC 12

**RESULT 13**

AW519844  
 LOCUS 660053H10.Y1 660 - Mixed stages of anther and pollen Zea mays cDNA, mRNA sequence.  
 DEFINITION  
 ACCESSION AW519844  
 VERSION AW519844.1 GI:7162237  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

**REFERENCE**  
**AUTHORS** Walbot,V.  
**TITLE** Maize ESTs from various cDNA libraries sequenced at Stanford  
**JOURNAL** University  
**COMMENT** Unpublished (1999)  
 Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 660053 row: H column: 10.  
**FEATURES**  
 source  
 1. 461  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="Ohio43"  
 /db\_xref="taxon:4577"  
 /tissue\_type="whole premeiotic anthers to pollen shed"  
 /dev\_stage="premeiotic anthers to pollen shed"  
 /lab\_host="XL0LR"  
 /clone\_lib="660 - Mixed stages of anther and pollen"  
 /note="Organ: anthers; Vector: Lambda Zap; Site 1: EcoRI; Site 2: XhoI; Anther and pollen cDNA library. Directionally sequenced with 5' end at the EcoRI site. Created by Amie Franklin."

**ORIGIN**

Query Match 95.1%; Score 276.6; DB 1; Length 461;  
 Best Local Similarity 96.9%; Pred. No. 8.6e-74;  
 Matches 282; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 60  
 Db 159 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 218  
 QY 61 GCAATGTGATCTGGAACTGCTGTTCTGGGTGGCGAGCTAGTATGACTGTGCTCAGTAA 120  
 Db 219 GCAATGTGATCTGGAACTGCTGTTCTGGGTGGCGAGCTGTTGTTATGACTGTGCTCAGTAA 278  
 QY 121 AATTTGGGGGCTCCCGGTATGAGATGCTGCGGGCAAGCCCTCGGTGCCACCTCGTTT 180  
 Db 279 AATTTGGGGGCTCCCGGTATGAGATGCTGCGGGCAAGCCCTCGGTGCCACCTCGTTT 338  
 QY 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGTTGGGTGGGAAGCCCTTTAAACTGTGTGCA 240  
 Db 339 GTGGCGGGGGCGCTGGAGCCCGGTCTGTTGGGTGGGAAGCCCTTTAAACTGTGTGCA 398  
 QY 241 CTTCATTTTACCTTTTCATCGCTGTTTATGAGTGGTCCCTATATCAA 291  
 Db 399 CTTCATTTTACCTTTTCATCGCTGTTTATGAGTGGTCCCAAAAAA 449

**RESULT 14**

DN217785  
 LOCUS DN217785  
 DEFINITION DN217785  
 ACCESSION DN217785  
 VERSION DN217785.1 GI:60350812  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 289)  
 Chen,H.D., Zhang,X., Zhou,R.L., Arias L.A.C., Shendelman,J.M., Zazubovits,N., Borsuk,L.A., Enrich,S.J., Ashlock,D.A., Scanlon,M.J. and Schnable,P.S.  
 Expressed Sequence Tags from B73 Maize Shoot Apical Meristems  
 Unpublished (2004)





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OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 23:00:44 ; Search time 122.379 Seconds  
(without alignments)  
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Title: US-10-603-524A-2

Perfect score: 291

Sequence: 1 agccggctttatgtcgtag.....tgtgagtggtcttatataca 291

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2\_6/prodata/1/ina/5 COMB.seq:\*
- 3: /cgn2\_6/prodata/1/ina/6A COMB.seq:\*
- 4: /cgn2\_6/prodata/1/ina/6B COMB.seq:\*
- 5: /cgn2\_6/prodata/1/ina/H COMB.seq:\*
- 6: /cgn2\_6/prodata/1/ina/PCUS COMB.seq:\*
- 7: /cgn2\_6/prodata/1/ina/PP COMB.seq:\*
- 8: /cgn2\_6/prodata/1/ina/RE COMB.seq:\*
- 9: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	34.6	11.9	1469	3	US-09-949-016-5398
C 2	34.6	11.9	75378	3	Sequence 5398, Ap
C 3	33.2	11.4	12787	3	Sequence 17140, A
4	32.4	11.1	516	3	Sequence 16359, A
5	32.4	11.1	846	3	Sequence 16362, A
6	32.4	11.1	885	3	Sequence 16471, A
C 7	31.8	10.9	103377	3	Sequence 16130, A
C 8	30.8	10.6	601	3	Sequence 16130, A
9	30.8	10.6	7381	3	Sequence 177958, A
10	30.4	10.4	25230	3	Sequence 16844, A
C 11	30.2	10.4	435	3	Sequence 13153, A
12	30.2	10.4	505	3	Sequence 2640, Ap
13	30.2	10.4	601	3	Sequence 15639, A
14	30.2	10.4	601	3	Sequence 17361, A
15	30.2	10.4	901	3	Sequence 149636, A
C 16	30.2	10.4	3798	3	Sequence 91, Appl
C 17	30.2	10.4	3839	3	Sequence 4204, Ap
C 18	30.2	10.4	156942	3	Sequence 485, App
C 19	30.2	10.4	156950	3	Sequence 12227, A
C 20	30	10.3	1023	3	Sequence 15946, A
C 21	30	10.3	2067	3	Sequence 5154, Ap
C 22	29.8	10.2	601	3	Sequence 11, Appl
C 23	29.8	10.2	1158	3	Sequence 150193, A
C 24	29.8	10.2	3109	3	Sequence 6363, Ap
					Sequence 413, App

C 25	29.8	10.2	90618	3	US-09-949-016-15964	Sequence 15964, A
C 26	29.6	10.2	858	3	US-09-252-991A-13905	Sequence 13905, A
C 27	29.6	10.2	1062	3	US-08-611-757-33	Sequence 33, Appl
C 28	29.6	10.2	1062	6	PCT-US95-05980-33	Sequence 33, Appl
C 29	29.6	10.2	1461	3	US-09-252-991A-13798	Sequence 13798, A
C 30	29.6	10.2	1656	3	US-09-252-991A-13545	Sequence 13545, A
C 31	29.6	10.2	8256	3	US-09-949-016-15951	Sequence 16951, A
C 32	29.6	10.2	80269	3	US-09-949-016-15681	Sequence 15681, A
C 33	29.4	10.1	1633	3	US-09-023-655-124	Sequence 124, App
C 34	29.4	10.1	57320	3	US-09-949-016-13983	Sequence 13983, A
C 35	29.2	10.0	474	3	US-09-621-976-18033	Sequence 18033, A
C 36	29.2	10.0	56302	3	US-09-949-016-11892	Sequence 11892, A
C 37	29	10.0	1391	3	US-09-270-767-13275	Sequence 13275, A
C 38	29	10.0	13164	3	US-09-949-016-11759	Sequence 11759, A
C 39	29	10.0	15165	3	US-09-949-016-15664	Sequence 15664, A
C 40	29	10.0	100463	3	US-09-949-016-12511	Sequence 12511, A
C 41	29	10.0	100468	3	US-09-949-016-13725	Sequence 13725, A
C 42	28.8	9.9	601	3	US-09-949-016-20694	Sequence 20694, A
C 43	28.8	9.9	1449	3	US-09-088-425-4	Sequence 4, Appl
C 44	28.8	9.9	1449	3	US-09-639-378A-4	Sequence 4, Appl
C 45	28.8	9.9	1762	3	US-09-799-451-622	Sequence 622, App

#### ALIGNMENTS

#### RESULT 1

US-09-949-016-5398/c  
; Sequence 5398, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5398  
; LENGTH: 1469  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-5398

Query Match 11.9%; Score 34.6; DB 3; Length 1469;  
Best Local Similarity 55.4%; Pred. No. 0.15;  
Matches 67; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY	93	CGACGCTAGTTATGACTGCTCGTCAGTAAATTTGGGGGCTCCCCGTATGAGATGCTGCGG	152
Db	151	CAAGGCCACTCATGGCATTGCTCTGAGGCTGGGGGCTCTCCAGGAGGATGATGACC	92
QY	153	GGCAAGGCTCGGTGTCCACCTCGTTTGTGGGGGGGGCGCTGGAGCCCGGCTCTGTTG	212
Db	91	GTGGCCCCCTGAAGGACGCCCTGGCGCTCTGAGGGGCGATGCTGAGCTGCGACTGTTGG	32
QY	213	G 213	
Db	31	G 31	

#### RESULT 2

US-09-949-016-17140/c  
; Sequence 17140, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17140  
LENGTH: 75378  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(75378)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-17140

Query Match 11.9%; Score 34.6; DB 3; Length 75378;  
Best Local Similarity 55.4%; Pred. No. 1.2;  
Matches 67; Conservative 0; Mismatches 54; Indels 0; Gaps 0;  
QY 93 CGACGCTAGTTATGACTGCTGCTAGTAAATTTGGGGGCTCCCCGTATGAGATGCTGCCG 152  
DB 2151 CAAGGCCACTCATGCAATTTGCTCTGAGGCTGGGGGCTCTCCAGGGAGATGATGACC 2092  
QY 153 GCAGAGGCTCGTGTCCACCTGCTTTTGGCGGGGGCGGTGAGCCCGTCTGGTTG 212  
DB 2091 GTGGCCCCCTGAAGACGCCCTGCGCCCTCTGGAGGGCATGCTGGAGCTGGCACTGGTGG 2032  
QY 213 G 213  
DB 2031 G 2031

RESULT 3  
US-09-949-016-16359  
Sequence 16359, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16359  
LENGTH: 12787  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-16359

Query Match 11.4%; Score 33.2; DB 3; Length 12787;  
Best Local Similarity 52.1%; Pred. No. 1.5;  
Matches 74; Conservative 0; Mismatches 68; Indels 0; Gaps 0;  
QY 128 GGGCTCCCGCTATGAGATGCTCCCGCAAGCCCTCGGTGTCCACCTCGTTTGGCGG 187  
DB 7738 GGGCACCTCTGTCAGAGCTCGGAGGAGGCTACCTGGCTACTACCTCCAGGGTAG 7797

QY 188 GGGGCGCTGGAGCCGGCTGCTGGTTGGTTGGAGCCCTTTAAACTGTTGTCACTTGCAT 247  
DB 7798 GTGGCGGGGGCCCTCCCTCCAGGGGGTTCCGAGTTCATTTGACCTTAGCCGCCCCAC 7857  
QY 248 TTTACCTTTTCCATCGCTGTTT 269  
DB 7858 TTTCTTTTCTTAAGCGAGTT 7879

RESULT 4  
US-09-252-991A-16362  
Sequence 16362, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 16362  
LENGTH: 516  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-16362

Query Match 11.1%; Score 32.4; DB 3; Length 516;  
Best Local Similarity 53.1%; Pred. No. 0.51;  
Matches 69; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
QY 77 CCTGTTTCTTGGGTGGCGAGCTAGTTATGACTGTCGTCAGTAAATTTGGGGGCTCCCC 136  
DB 91 CCTGGGCTCTTGGCGGGCGCTGGCTGCTGGACAGACCCCTGCTTGTGCGGCCAC 150  
QY 137 GTATGAGATGCTGCGGGCGAGGCTCGGTGTCCACCTCGTTTGTGCGGGGGCGCTG 196  
DB 151 CCTGGCGCGCTGCTGGCCCTGGCGGATGGCGGCTGAGGGTTGCGGTTGCGCGC 210  
QY 197 GAGCCCGGTC 206  
DB 211 GGGAGAGGCG 220

RESULT 5  
US-09-252-991A-16471  
Sequence 16471, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 16471  
LENGTH: 846  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-16471

Query Match 11.1%; Score 32.4; DB 3; Length 846;  
Best Local Similarity 53.1%; Pred. No. 0.66;



Matches 69; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
QY 77 CTGTTCTTCTGGTGGCGAGCGCTAGTATGATCGTCAGTAAATTTGGGGCTCCCC 136  
Db 303 CTGGGCTCTGGCGCGCGCTGCTCTCCCTGAGACAAGCCCTGTGTCGCGCCAC 362  
QY 137 GTATGAGATGCTGCCGGCAAGCCCTCGGTGTCACACCTCGTTTGGCGGGGGCGCTG 196  
Db 363 CCTCGCCCGCTGCTGGCCCTGCGCGGATGGCGCGCTGGAGGGTTCCCGGTTCGCGCG 422  
QY 197 GAGCCCGGTC 206  
Db 423 GCGAGAGGCG 432

## RESULT 6

US-09-252-991A-16130/c  
; Sequence 16130, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 16130  
; LENGTH: 885  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-16130

Query Match 11.1%; Score 32.4; DB 3; Length 885;  
Best Local Similarity 53.1%; Pred. No. 0.68;  
Matches 69; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 77 CTGTTCTTCTGGTGGCGAGCGCTAGTATGATCGTCAGTAAATTTGGGGCTCCCC 136  
Db 487 CTGGGCTCTGGCGCGCGCTGCTCTCCCTGAGACAAGCCCTGTGTCGCGCCAC 428  
QY 137 GTATGAGATGCTGCCGGCAAGCCCTCGGTGTCACACCTCGTTTGGCGGGGGCGCTG 196  
Db 427 CCTCGCCCGCTGCTGGCCCTGCGCGGATGGCGCGCTGGAGGGTTCCCGGTTCGCGCG 368  
QY 197 GAGCCCGGTC 206  
Db 367 GCGAGAGGCG 358

## RESULT 7

US-09-949-016-14089  
; Sequence 14089, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14089  
; LENGTH: 103377  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(103377)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14089

Query Match 10.9%; Score 31.8; DB 3; Length 103377;  
Best Local Similarity 59.3%; Pred. No. 14;  
Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
QY 12 TGTGCGTAGAACTAGTAGTCTTTGCTGCTCGAATGACACTATGCAATGTGATC 71  
Db 73138 TGTGCTAAATGTCAAAAGTTGTGTTGCTGTTGAAGGCCACTTTGCAATGCTCCC 73197  
QY 72 TCGAACCTGGTTCTTGGGTGCGGACGCTAGT 102  
Db 73198 TAGAACTTGGGTATGTGGCGAGGAGATGGT 73228

## RESULT 8

US-09-949-016-177958/c  
; Sequence 177958, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 177958  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-177958

Query Match 10.6%; Score 30.8; DB 3; Length 601;  
Best Local Similarity 54.4%; Pred. No. 2;  
Matches 62; Conservative 0; Mismatches 52; Indels 0; Gaps 0;  
QY 125 TGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGCCCTCGGTGTCACCTCGCTTTGTGG 184  
Db 482 TGGGGGTAGCAGGTTTGAGATGCTGTCGGGTGTCAGGCCAGCCCTAGGCTCAGC 423  
QY 185 CGGGGGCGCTGGAGCCCGGCTCGTTGGGTGGAGCCCTTTAAACTGTGT 238  
Db 422 TGTGGAGGAGAACGCTGGGCCCGGGGCGCTGGGTGTCCTGAAGCTCCTGT 369

## RESULT 9

US-09-949-016-16844  
; Sequence 16844, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755

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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16844
; LENGTH: 7381
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)...(7381)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-16844

Query Match      10.6%; Score 30.8; DB 3; Length 7381;
Best Local Similarity 54.4%; Pred. No. 7.6;
Matches 62; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 125 TGGGGCTCCCGTATGAGTGTGCGGGCAAGCCCTCGGTGCCACCTGCTTTGGG 184
Db 3731 TGGGGTAGCAGGTTTGAGTGTCTGCGGTGCTGGGTCCAGGCCAGGCTAGGCTCAGC 3790

Qy 185 CGGGGGCGCTGGAGCCCGTCTGTTGGTTGGGAAGCCCTTTAAACTGTGT 238
Db 3791 TGTGGGAGGAGAACGCTGGCGCGGGAGGCGCTGGGTGTCCCTGAAGCTCCTGT 3844

RESULT 10
US-09-949-016-13153
; Sequence 13153, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13153
; LENGTH: 25230
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-13153

Query Match      10.4%; Score 30.4; DB 3; Length 25230;
Best Local Similarity 63.9%; Pred. No. 20;
Matches 46; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 69 ATCTGGAACCTGTTTCTTTGGGTGCGACGCTAGTTATGACTGCTCAGTAAATTTGGG 128
Db 13804 ATATACATCTCTGGTTGCTGGGGGATACCACTTTATGCTGTGCTCAGGCATAATTAAC 13863

Qy 129 GGCTCCCGGTAT 140
Db 13864 AGCACCCCTTTT 13875

RESULT 11
US-09-134-001C-2640/c
; Sequence 2640, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
```

```
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2640
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-2640

Query Match      10.4%; Score 30.2; DB 3; Length 435;
Best Local Similarity 69.5%; Pred. No. 2.7;
Matches 41; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 209 GTTGGTTGGGAAGCCCTTTAAACTGTGTGCTGCTGCTTTTACCTTTTCCATCGTGT 267
Db 192 GTTAGGGTGTGAACATCGATAGACTTTTATCCATTCACTTTTACCTTTTCCATATCTGT 134

RESULT 12
US-09-621-976-15639
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Wilne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15639
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-15639

Query Match      10.4%; Score 30.2; DB 3; Length 505;
Best Local Similarity 11.2%; Pred. No. 3;
Matches 28; Conservative 121; Mismatches 99; Indels 1; Gaps 1;

Qy 22 AACTAGTAGTAGTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 81
Db 1 AMAYMSSRYRTSSKSKRYGKYSMYSRWSMKYAWGCRGKYGTSGRCGRGSRGSMCKSWG 60

Qy 82 TTCTCTGGTGGACGCTAGTTATGACTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 141
Db 61 YRYSYMGYKWSKWSKMKKYSKRGMTSKSTRTKRYTYSKCRKTCTCKYRGWSWKRWKWR 120

Qy 142 AGATGC-TGCCGGGCAAGCCCTCGGTGTCCACCTCGTTTGTGGCGGGGGCGCTGGAGC 200
Db 121 RKMYYRMKYSKASYSYRRCRKYTGTRGWYGCCKRMCKSSRYMTRYRYMKMTGA 180

Qy 201 CCGGTCTGTTGGGTGGGAAGCCCTTAAACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 260
Db 181 CYGSKGMSCKGRSKYGSWKWYTKYTMCTSKYKSKMSKYSKYSKSMCYTYMMCYTYWMC 240

Qy 261 TCGCTGTTT 269
Db 241 TCTYKKSYY 249

RESULT 13
US-09-949-016-27361
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RESULT 15
US-09-311-021-91
; Sequence 91, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Pechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 901
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-311-021-91

```

	Query Match Best Local Similarity Matches	10.4% 55.1% 59;	Score 30.2; Pred. No. 4; Conservative 0;	Mismatches 48;	Indels 0;	Gaps 0;
Qy	103	TATGACTGTCGT	CAGTAAATTTGGGGGCTCCCGGTATGAGATCTGCGGGGCAAGGCCT	162		
Db	527	TGTCCTCTCAGCAGACACAGTTCCAGTGCTCTCTGGCAGAACTGAAGCAGGCCACAGACC	586			
Qy	163	CGGTGTCCCACTCGTTTGTGTGGGGGGGGCGCTGGAGCCCGGTCTGG	209			
Db	587	TGATGAGCTCCCTGGGCTGAGAGAAAGGTGTTCACGCTGTGTGG	633			

Search completed: March 7, 2006, 23:09:18  
Job time : 124.379 secs

	Query Match	10.4%	Score 30.2;	DB 3;	Length 601;
	Best Local Similarity	62.7%;	Pred. No. 3.3;		
	Matches	47;	Conservative	0;	Mismatches 28; Indels 0; Gaps 0;
QY	212	GGGTGGGAAGCCCTTTAAACTGTGTGCATTCGATTTTCCATCGCTGTTTAT	271		
Db	487	GGGTTCAGAGTCGCTTAAAAAGTTTGTGCACATCTTTTACATTTCTAGGGTTCTCTTCAG	546		

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Result No.	Query			Description		
	Score	Match	Length	ID	DB	
1	183.2	63.0	1252	9	US-11-096-568A-16048	Sequence 16048, A
2	33.4	11.5	599	6	US-09-925-065A-705105	Sequence 705105, A
3	32.8	11.3	201	12	US-11-124-367A-21598	Sequence 21598, A
4	32.6	11.2	553	6	US-09-925-065A-10284	Sequence 10284, A
5	32.6	11.2	553	6	US-09-925-065A-10285	Sequence 10285, A
6	32.2	11.1	553	6	US-09-925-065A-10286	Sequence 10286, A
7	31.4	10.8	656	6	US-09-925-065A-88099	Sequence 88099, A
8	31.2	10.7	372	12	US-11-037-243-18	Sequence 18, Appl
9	30	10.3	566	6	US-09-925-065A-457896	Sequence 457896, A
10	30	10.3	629	6	US-09-925-065A-916170	Sequence 916170, A
11	30	10.3	634	6	US-09-925-065A-915272	Sequence 915272, A
12	30	10.3	10000	12	US-11-124-368A-2913	Sequence 2913, Appl
13	29.8	10.2	630	6	US-09-925-065A-788291	Sequence 788291, A
14	29.8	10.2	1149	6	US-09-925-065A-709944	Sequence 709944, A
15	29.8	10.2	1785	8	US-10-750-185-50507	Sequence 50507, A
16	29.8	10.2	1785	8	US-10-750-623-50507	Sequence 50507, A
17	29.6	10.2	7001	12	US-11-011-332A-75	Sequence 75, Appl
18	29.6	10.2	8252	12	US-11-011-332A-150	Sequence 150, Appl
19	29.2	10.0	446	6	US-09-925-065A-36828	Sequence 36828, A
20	29	10.0	608	6	US-09-925-065A-735119	Sequence 735119, A

Db 1175 TTAAACTGTGTGCGTTGCAATTTTAACTTTTCATCGCGTTCAGTGGTCTTAATCTAT 1234  
|||||

## RESULT 2

US-09-925-065A-705105/c  
; Sequence 705105, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 705105

; LENGTH: 599

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-705105

Query Match 11.5%; Score 33.4; DB 6; Length 599;

Best Local Similarity 48.7%; Pred. No. 1;

Matches 91; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 36 GTTCTCTGTCGATGACATGCACTATGATGATCTGGAACCTGGTTCTTGGTGCGA 95

Db 526 GGTTCCTGTTGGGGAGGCCCTGGATCTATGCTGTAGAAACATTTCTTCTGTGCC 467

QY 96 CCTAGTTATGATCTGCTGCTAGTAAATTTGGGGGCTCCCCATGAGATGCTGCCGGGC 155

Db 466 CTTGAGTGAGCCCTTCCAGAGAAAATCAGAAAGTCAGGCCCAAGATCTATGCT 407

QY 156 AAGGCTCGGTGTCACCTCTTTGTGGCGGGGGCGCTGAGCCCGTCTGGTTGGGT 215

Db 406 TCTCTCCAGTATCCAAACATACTAGATTTCAGAGGGGTTGGAGACAGGCAATCCTGGCT 347

QY 216 TGGGAAG 222

Db 346 ACTGAAG 340

## RESULT 3

US-11-124-367A-21598  
; Sequence 21598, Application US/11124367A  
; Publication No. US20060024700A1  
; GENERAL INFORMATION:

; APPLICANT: Michele Cargill

; APPLICANT: Honglin Huang

; TITLE OF INVENTION: Genetic Polymorphisms Associated with

; Fibrosis Methods of Detection and Uses Thereof

; FILE REFERENCE: CL001519.ORD

; CURRENT APPLICATION NUMBER: US/11/124,367A

; CURRENT FILING DATE: 2005-05-09

; PRIOR APPLICATION NUMBER: US 60/568,846

; PRIOR FILING DATE: 2004-05-07

; PRIOR APPLICATION NUMBER: US 60/582,609

; PRIOR FILING DATE: 2004-06-25

; PRIOR APPLICATION NUMBER: US 60/599,554

; PRIOR FILING DATE: 2004-08-09

; NUMBER OF SEQ ID NOS: 34460

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 21598

; LENGTH: 201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-124-367A-21598

Query Match 11.3%; Score 32.8; DB 12; Length 201;

Best Local Similarity 58.5%; Pred. No. 1.1;

Matches 55; Conservative 1; Mismatches 38; Indels 0; Gaps 0;

QY 121 AATTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGGCCTCGGTGTCCACCTCGTTT 180

Db 59 AATGAGGCGCTGCCGGGACCTCTCTCCACCAATCCCGMGTCGTCACCCCTGCTT 118

QY 181 GTGGGGGGGGCGCTGAGCCCGTCTGTTGGG 214

Db 119 GGGGTCCGGGCTCTGGGGTCTGCTAGGCTGGG 152

## RESULT 4

US-09-925-065A-10284/c

; Sequence 10284, Application US/09925065A

; Publication No. US20040181048A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10284

; LENGTH: 553

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-10284

Query Match 11.2%; Score 32.6; DB 6; Length 553;

Best Local Similarity 52.6%; Pred. No. 1.8;

Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 3 CCGGCTTTATGTGGGTAGAAACTAGTAGTGTGTTCTGCTGTCGATGACATATGC 62

Db 236 CCTACTTTGTAAGCCATAAATCTCTGGCTCTCTTGGTTCTAATGACCCAGGAGACTCTTC 177

QY 63 AATGATCTCGAACCCTGTTTCTTGGGTGCGAGCGTAGTATGACTGTCGTCAGTAAA 122

Db 176 AATGACATTTGGATTCGTTTCTCTGGGAGCTTTCTCTTAATCTGGGATACCTCAA 117

QY 123 TTGGGGGCTCCCG 137

Db 116 GTGTAAGCCAGCCTG 102

## RESULT 5

US-09-925-065A-10285/c

; Sequence 10285, Application US/09925065A

; Publication No. US20040181048A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

[illegible]

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; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 3372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-037-243-18

Query Match          10.7%; Score 31.2; DB 12; Length 3372;
Best Local Similarity 57.0%; Pred. No. 9.7;
Matches 57; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 141 GAGATGCTGCCGGCGAAGCCCTCGGTGTCCACCTCGTTTGGCGGGGGCGCTGGAGC 200
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 261 GAGCTGGGGCTGGGTCCGGGCGGGGCTTCCTCCCGGGGCTCCCGGGGCGCTGGAC 202
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 201 CCGGTCTGGTTGGTGGGAAGCCCTTTAAACTGTTGTCA 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 201 TGGGCGCGGGCGCAGCGAAGCCGCCCTCACCGTCGCCA 162
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
US-09-925-065A-457896
; Sequence 457896, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457896
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-457896

Query Match          10.3%; Score 30; DB 6; Length 566;
Best Local Similarity 57.4%; Pred. No. 13;
Matches 54; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 79 TGGTTCTTGGGTGGCGACCTAGTTATGACTGTCGTCACTAAATTTGGGGGCTCCCGGT 138
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 163 TGCCTCTCTGAGCAAAAGTGTTCACACTCTGGCCCTTCCACGGTGGTGGTCTCTCA 222
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 139 ATGAGATGCTCGCGGCAAGGCTCGGTGTCCCA 172
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 223 CITAGATGCTGCTGGGAAGCCCTTAGAGTCCCA 256
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
US-09-925-065A-916170
; Sequence 916170, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A

; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 916170
; LENGTH: 629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-916170

Query Match          10.3%; Score 30; DB 6; Length 629;
Best Local Similarity 53.4%; Pred. No. 13;
Matches 63; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 8 TTTATGTGCGTAGAAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTATGCAATGT 67
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 29 TTTATTTTCACATAAAATGTAGATTGCTATTGACATTTTCACATAGCAATTATGTTAATT 88
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 68 GATCTGGAACTGGTTCTTCGGGTGGCGACGCTAGTATGACTGTGTCGTCAGTAAATTT 125
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 89 CATATGGAATTTGAAATCTGGGAGTTTAACTTCTCTTTCTGTTTTTCATTATATTT 146
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-09-925-065A-915272/c
; Sequence 915272, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 915272
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-915272

Query Match          10.3%; Score 30; DB 6; Length 634;
Best Local Similarity 53.4%; Pred. No. 13;
Matches 63; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 8 TTTATGTGCGTAGAAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTATGCAATGT 67
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 620 TTTATTTTCACATAAAATGTAGATTGCTATTGACATTTTCACATAGCAATTATGTTAATT 561
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 68 GATCTGGAACTGGTTCTTCGGGTGGCGACGCTAGTATGACTGTGTCGTCAGTAAATTT 125
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 560 CATATGGAATTTGAAATCTGGGAGTTTAACTTCTCTTTCTGTTTTTCATTATATTT 503
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 12  
US-11-124-368A-2913/c  
; Sequence 2913, Application US/11124368A  
; Publication No. US20050287559A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: James J. Devlin  
; APPLICANT: May Luke  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof  
; FILE REFERENCE: CL001524  
; CURRENT APPLICATION NUMBER: US/11/124,368A  
; CURRENT FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,845  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/625,936  
; PRIOR FILING DATE: 2004-11-09  
; NUMBER OF SEQ ID NOS: 21112  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2913  
; LENGTH: 100000  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-124-368A-2913

Query Match 10.3%; Score 30; DB 12; Length 100000;  
Best Local Similarity 52.4%; Pred. No. 79;  
Matches 66; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
Qy 152 GGGCAAGCCCTCGGTCCACCTGTTGTGGGGGGGGCTGGAGCCCGGTCTGTT 211  
Db 1981 GGGAGGGTCCCGGGGAGCTGGGGGGTGGGCTGGGGGGCTGTTTGGGC 1922  
Qy 212 GGGTTGGGAAGCCCTTTAAACTGTGTCACTTGCACTTTTACCTTTTCCATCGCTGTTAT 271  
Db 1921 TGGAGCGTCCCGGGTGTGTGTGTACTGGGAGGTGAGCTTCTGCTGGGATTG 1862  
Qy 272 TGTGAG 277  
Db 1861 TGTGAG 1856

RESULT 13  
US-09-925-065A-788291/c  
; Sequence 788291, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 788291  
; LENGTH: 630  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-788291

Query Match 10.2%; Score 29.8; DB 6; Length 630;

Best Local Similarity 55.2%; Pred. No. 15;  
Matches 58; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
Qy 3 CCGGCTTTATGTCGTAGAAAAGTAAGTAGTGTGTCGTGTCGAATGACATATGC 62  
Db 508 CAGGGATTATGTCGAGCGTAACCATCACAACACTTGCATCGGAGATTCTTATCTTCA 449  
Qy 63 AATGTGATCTGGAACCTGTTTCTTGGGTGGAGCGCTAGTTATGA 107  
Db 448 ACTCTGATCTTAAACTGCTTCTTCTGGAGTGTCTAGATAAGGATAA 404

RESULT 14  
US-09-925-065A-709944/c  
; Sequence 709944, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 709944  
; LENGTH: 1149  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-709944

Query Match 10.2%; Score 29.8; DB 6; Length 1149;  
Best Local Similarity 52.0%; Pred. No. 19;  
Matches 64; Conservative 1; Mismatches 58; Indels 0; Gaps 0;  
Qy 152 GGGCAAGCCCTCGGTCCACCTGTTGTGGGGGGGGCTGGAGCCCGGTCTGTT 211  
Db 669 GTGTGAGACCTTGTCTCCCAACCTTGATTCAGGAACCTGAGGATGGGATGKGTG 610  
Qy 212 GGGTTGGGAAGCCCTTTAAACTGTGTCACTTTTACCTTTTCCATCGCTGTTAT 271  
Db 609 GGGTTGGGTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 550  
Qy 272 TGT 274  
Db 549 TTT 547

RESULT 15  
US-10-750-185-50507/c  
; Sequence 50507, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185

Wed Mar 8 09:43:21 2006

```

; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50507
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Bovine 19866880889331
US-10-750-185-50507

Query Match      10.2%; Score 29.8; DB 8; Length 1785;
Best Local Similarity 60.5%; Pred. No. 22;
Matches 49; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 102 TTATGACTGTGCTCAGTAAATTTGGGGGCTCCCGGTATGAGATGCTGCCGGGCAAGGCC 161
Db 740 TTAGGTTTGTAGTCAATTAAAATCTGGACTACCCACATGCTATGCTGGGAGCTTGGTC 681

Qy 162 TCGGTGTCCCACTCGTTGT 182
Db 680 TCTGCCATTCAATGTATTAT 660

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Search completed: March 8, 2006, 06:10:11  
Job time : 776.844 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 04:11:07 ; Search time 629.177 Seconds  
(without alignments)  
3824.664 Million cell updates/sec

Title: US-10-603-524A-2

Perfect score: 291

Sequence: 1 agccggctttatgtcgttag.....tgtgagtggtctctatatcaa 291

Scoring table: IDENTIFY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA\_Main:

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	291	100.0	291	7	US-10-603-524A-2
2	285.8	98.2	653	7	US-10-425-114-19731
3	285.8	98.2	1283	7	US-10-425-114-21156
4	260.2	89.4	733	7	US-10-425-114-32231
5	258.2	88.7	689	7	US-10-425-114-20758
6	253.2	87.0	752	7	US-10-425-114-32479
7	245.8	84.5	487	7	US-10-425-114-17184
8	221.4	76.1	267	7	US-10-424-599-14742
9	218.6	75.1	394	8	US-10-425-115-6597
10	217	74.6	1270	7	US-10-767-701-15432
11	206.2	70.9	464	8	US-10-425-115-153129
12	195.2	67.1	807	7	US-10-425-114-15469
13	195.2	67.1	824	7	US-10-425-114-25681
14	195.2	67.1	969	7	US-10-425-114-26556
15	195.2	67.1	1114	8	US-10-425-115-6593
16	189.6	65.2	283	8	US-10-425-115-75283
17	177.2	60.9	383	8	US-10-425-115-119075
18	172.2	59.2	378	8	US-10-425-115-14719
19	172.2	59.2	394	8	US-10-425-115-123144
20	170.2	58.5	385	8	US-10-425-115-162596
21	163.8	56.3	219	8	US-10-425-115-70427
22	160.2	55.1	303	8	US-10-425-115-147735
23	159.6	54.8	361	8	US-10-425-115-119871

#### ALIGNMENTS

##### RESULT 1

US-10-603-524A-2  
; Sequence 2, Application US/10603524A  
; Publication No. US20040158887A1  
; GENERAL INFORMATION:  
; APPLICANT: Dow AgroSciences LLC  
; TITLE OF INVENTION: USE OF REGULATORY SEQUENCES IN TRANSGENIC PLANTS  
; FILE REFERENCE: 50528A  
; CURRENT APPLICATION NUMBER: US/10/603,524A  
; CURRENT FILING DATE: 2003-06-25  
; PRIOR FILING DATE: 60/392571  
; PRIOR FILING DATE: 2002-06-27  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 291  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-10-603-524A-2

Query Match 100.0%; Score 291; DB 7; Length 291;

Best Local Similarity 100.0%; Pred. No. 3.8e-87;

Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AGCGGCTTTATGTCGTAGAACTAGTAGTAGTGTGCTGTCGAATGACACTAT	60
Db	1	AGCGGCTTTATGTCGTAGAACTAGTAGTAGTGTGCTGTCGAATGACACTAT	60
Qy	61	GCAATGTCATCTGGAACCTGCTTCTCGGTGCGACGCTAGTATGCTGTCAGTAA	120
Db	61	GCAATGTCATCTGGAACCTGCTTCTCGGTGCGACGCTAGTATGCTGTCAGTAA	120
Qy	121	AATTGGGGGCTCCCGGTATGAGATGTCGCGGCAAGCCCTCGGTGCCACCTCGTTT	180
Db	121	AATTGGGGGCTCCCGGTATGAGATGTCGCGGCAAGCCCTCGGTGCCACCTCGTTT	180
Qy	181	GTGGCGGGGGCGCTGGAGCCCGGTCTGGTGGGTGGGAAGCCCTTTAAACTGTGTCA	240
Db	181	GTGGCGGGGGCGCTGGAGCCCGGTCTGGTGGGTGGGAAGCCCTTTAAACTGTGTCA	240
Qy	241	CTTGCAATTTACCTTTTCCATCGCTGTTTATGAGTGGTCCCTATATCAAA	291
Db	241	CTTGCAATTTACCTTTTCCATCGCTGTTTATGAGTGGTCCCTATATCAAA	291

##### RESULT 2

US-10-425-114-19731  
; Sequence 19731, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 19731  
; LENGTH: 653  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3150-117-G4\_FLI  
US-10-425-114-19731

Query Match 98.2%; Score 285.8; DB 7; Length 653;  
Best Local Similarity 99.3%; Pred. No. 2.8e-85;  
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGCCGGCTTTATGTCGTAGAAACTAGTAGCTAGTGTGCTGTGTCGAATGACACTAT 60  
DB 365 AGCCGGCTTTATGTCGTAGAAACTAGTAGCTAGTGTGCTGTGTCGAATGACACTAT 424  
QY 61 GCAATGATCTGGAACCTGTTCTTGGGTGCGACCGCTAGTATGACTGTCGTCAGTAA 120  
DB 425 GCAATGATCTGGAACCTGTTCTTGGGTGCGACCGCTTGTATGACTGTCGTCAGTAA 484  
QY 121 AATTGGGGGCTCCCGCTATGAGATGCTGCGGGCAAGCCCTCGGTGTCACCTCGTT 180  
DB 485 AATTGGGGGCTCCCGCTATGAGATGCTGCGGGCAAGCCCTCGGTGTCACCTCGTT 544  
QY 181 GTGCGGGGGCGCTGGAGCCCGCTCTGTTGGGTGGGAAGCCCTTTAAACTGTTGTCA 240  
DB 545 GTGCGGGGGCGCTGGAGCCCGCTCTGTTGGGTGGGAAGCCCTTTAAACTGTTGTCA 604  
QY 241 CTTCGATTTTACCTTTTCCATCGCTGTTTATGAGTGGTCTCTATATC 289  
DB 605 CTTCGATTTTACCTTTTCCATCGCTGTTTATGAGTGGTCTCTATATC 653

RESULT 3  
US-10-425-114-21156  
; Sequence 21156, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 21156  
; LENGTH: 1283  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3279-175-F1\_FLI  
US-10-425-114-21156

Query Match 98.2%; Score 285.8; DB 7; Length 1283;  
Best Local Similarity 99.3%; Pred. No. 3.6e-85;  
Matches 287; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGCCGGCTTTATGTCGTAGAAACTAGTAGCTAGTGTGCTGTGTCGAATGACACTAT 60  
DB 995 AGCCGGCTTTATGTCGTAGAAACTAGTAGCTAGTGTGCTGTGTCGAATGACACTAT 1054  
QY 61 GCAATGATCTGGAACCTGTTCTTGGGTGCGACCGCTAGTATGACTGTCGTCAGTAA 120  
DB 1055 GCAATGATCTGGAACCTGTTCTTGGGTGCGACCGCTTGTATGACTGTCGTCAGTAA 1114  
QY 121 AATTGGGGGCTCCCGCTATGAGATGCTGCGGGCAAGCCCTCGGTGTCACCTCGTT 180  
DB 1115 AATTGGGGGCTCCCGCTATGAGATGCTGCGGGCAAGCCCTCGGTGTCACCTCGTT 1174  
QY 181 GTGCGGGGGCGCTGGAGCCCGCTCTGTTGGGTGGGAAGCCCTTTAAACTGTTGTCA 240  
DB 1175 GTGCGGGGGCGCTGGAGCCCGCTCTGTTGGGTGGGAAGCCCTTTAAACTGTTGTCA 1234  
QY 241 CTTCGATTTTACCTTTTCCATCGCTGTTTATGAGTGGTCTCTATATC 289  
DB 1235 CTTCGATTTTACCTTTTCCATCGCTGTTTATGAGTGGTCTCTATATC 1283

RESULT 4  
US-10-425-114-32231  
; Sequence 32231, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 32231  
; LENGTH: 733  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-ZMFLB73277A08\_FLI  
US-10-425-114-32231  
Query Match 89.4%; Score 260.2; DB 7; Length 733;  
Best Local Similarity 94.6%; Pred. No. 1.2e-76;  
Matches 283; Conservative 0; Mismatches 8; Indels 8; Gaps 1;  
QY 1 AGCCGGCTTTATGTCGTAGAAACTAGTAGCTAGTGTGCTGTGTCGAATGACACTAT 60  
DB 396 AGCCGGCTTTATGTCGTAGAAACTAGTAGCTAGTGTGCTGTGTCGAATGACACTAT 455  
QY 61 GCAATGATCTGGAACCTGTTCTTGGGTGCGACCGCT-----AGTTATGACTGTC 112  
DB 456 GCAATGATCTGGAACCTGTTCTTGGGTGCGACCGCTTGTAGCCGTTGTTATGACTGTC 515  
QY 113 GTGAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCGGGCAAGCCCTCGGTGTCCA 172  
DB 516 GTCCGTAATAATTTGGGGGCTCCCGTAAAGGATGCTGCTCGCAAGGCCCTCGGTGTCCA 575  
QY 173 CCTCGTTTGTGCGGGGGCGCTGGAGCCCGCTCTGTTGGGTGGGAAGCCCTTTAAAC 232  
DB 576 CCTCGTGTGCGGGGGCGCTGGAGCCCGCTCTGTTGGGTGGGAAGGCCCTTTAAAC 635  
QY 233 TGTGTGCACTTGTGCAATTTTACCTTTTCCATCGCTGTTTATGAGTGGTCTCTATATCA 291

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Db 636 TGTGTCACTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTATATCAA 694
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73376G05_FLI
US-10-425-114-32479

RESULT 5
US-10-425-114-20758
; Sequence 20758, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 20758
; LENGTH: 689
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3245-170-A6_FLI
US-10-425-114-20758

Query Match 88.7%; Score 258.2; DB 7; Length 689;
Best Local Similarity 94.6%; Pred. No. 5.4e-76;
Matches 281; Conservative 0; Mismatches 8; Indels 8; Gaps 1;

QY 1 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGTTGCTGCTGCTGCGAATGACACTAT 60
Db 393 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGTTGCTGCTGCTGCGAATGACACTAT 452

QY 61 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCT-----AGTTATGACTGTC 112
Db 453 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCTTTGAGCGGTGTTATGACTGTC 512

QY 113 GTCAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCGGCGAAGGCTCGGTGTCCTCA 172
Db 513 GTCAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCGGCGAAGGCTCGGTGTCCTCA 572

QY 173 CTTGCTGTTGCGGGGGCGCTGGAGCCGCTCTGTTGGTGGGAGCCCTTTAAAC 232
Db 573 CTTGCTGTTGCGGGGGCGCTGGAGCCGCTCTGTTGGTGGGAGCCCTTTAAAC 632

QY 233 TGTGTCACTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTATATC 289
Db 633 TGTGTCACTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCTATATC 689

RESULT 6
US-10-425-114-32479
; Sequence 32479, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32479
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-038-B11_FLI
US-10-425-114-17184

Query Match 84.5%; Score 245.8; DB 7; Length 487;
Best Local Similarity 99.2%; Pred. No. 7e-72;
Matches 247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGTTGCTGCTGCGAATGACACTAT 60
Db 239 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGTTGCTGCTGCGAATGACACTAT 298

QY 61 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAA 120
Db 299 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAA 358

QY 121 AATTGGGGGCTCCCGGTATGAGATGCTGCGGCGAAGCCCTCGGTGTCCTCGTTT 180
Db 359 AATTGGGGGCTCCCGGTATGAGATGCTGCGGCGAAGCCCTCGGTGTCCTCGTTT 418

QY 181 GTGCGGGGGCGCTGGAGCCGCTGCTGTTGGGTGGGAGGCCCTTTAAACCTGTTGCA 240
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; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73376G05_FLI
US-10-425-114-32479

Query Match 87.0%; Score 253.2; DB 7; Length 752;
Best Local Similarity 94.5%; Pred. No. 2.7e-74;
Matches 276; Conservative 0; Mismatches 8; Indels 8; Gaps 1;

QY 1 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGTTGCTGCTGCGAATGACACTAT 60
Db 461 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGTTGCTGCTGCGAATGACACTAT 520

QY 61 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCT-----AGTTATGACTGTC 112
Db 521 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCTTTGAGCCGTGTTATGACTGTC 580

QY 113 GTCAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCGGCGAAGGCTCGGTGTCCTCA 172
Db 581 GTCAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCGGCGAAGGCTCGGTGTCCTCA 640

QY 173 CTTGCTGTTGCGGGGGCGCTGGAGCCGCTCTGTTGGTGGGAGCCCTTTAAAC 232
Db 641 CTTGCTGTTGCGGGGGCGCTGGAGCCGCTCTGTTGGTGGGAGCCCTTTAAAC 700

QY 233 TGTGTCACTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCT 284
Db 701 TGTGTCACTTGCAATTTTACCTTTTCCATCGCTGTTTATTGTGAGTGGTCCT 752

RESULT 7
US-10-425-114-17184
; Sequence 17184, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 17184
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-038-B11_FLI
US-10-425-114-17184

Query Match 84.5%; Score 245.8; DB 7; Length 487;
Best Local Similarity 99.2%; Pred. No. 7e-72;
Matches 247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGTTGCTGCTGCGAATGACACTAT 60
Db 239 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGTTGCTGCTGCGAATGACACTAT 298

QY 61 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAA 120
Db 299 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCTAGTTATGACTGTCGTCAGTAA 358

QY 121 AATTGGGGGCTCCCGGTATGAGATGCTGCGGCGAAGCCCTCGGTGTCCTCGTTT 180
Db 359 AATTGGGGGCTCCCGGTATGAGATGCTGCGGCGAAGCCCTCGGTGTCCTCGTTT 418

QY 181 GTGCGGGGGCGCTGGAGCCGCTGCTGTTGGGTGGGAGGCCCTTTAAACCTGTTGCA 240
```

Db 419 GTGGCGGGGGCGCTGGAGCCCGGTCTGGTTGGGTTGGGAAGCCCTTTAAACTGTTGTCA 478

Qy 241 CTTGCAATTT 249

Db 479 CTTGCAATTT 487

#### RESULT 8

US-10-424-599-14742

; Sequence 14742, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 14742

; LENGTH: 267

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MBT3847\_113318C.1

US-10-424-599-14742

Query Match 76.1%; Score 221.4; DB 7; Length 267;

Best Local Similarity 92.8%; Pred. No. 9e-64;

Matches 246; Conservative 0; Mismatches 11; Indels 8; Gaps 1;

Qy 14 TCGGTAGAACTAGTAGCTAGTGGTTGCTGCTGCTGCAATGACACTATGCAATGTGATCTG 73

Db 1 TGCCTAGAACTAGTAGCTAGTGGTTGCTGCTGCTGCAATGACACTATGCAATGTGATCTG 60

Qy 74 GAACCTGGTTCTCGGTGGCGACGCT-----AGTTATGACTGCTGCTCAGTAAATTT 125

Db 61 GAACCTGGTTCTCGGTGGCGACGCTGTGAGCCGTGTATGACTGTGCTGCGTAAATTT 120

Qy 126 GGGGGCTCCCTATGAGATGCTGCGGCAAGGCTCGGTGTCCTCCACTCTGTTGTGCGC 185

Db 121 GGGGGCTCCCTATGAGATGCTGCTGCAAGGCTCGGTGTCCTCCACTCTGTTGTGCGC 180

Qy 186 GGGGGCGCTGAGCCCGGTCTGGTTGGTTGGGAAGCCCTTTAAACTGTTGTCACTTGC 245

Db 181 GTGGGGCGCTGAGCCCGGTCTGGTTGGTTGGGAAGCCCTTTAAACTGTTGTCACTTGC 240

Qy 246 ATTTTACCTTTTCCATCGCTGTTTA 270

Db 241 ATTTTACCTTTTCCATCGCTGTTAA 265

#### RESULT 9

US-10-425-115-6597

; Sequence 6597, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 6597

; LENGTH: 394

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577\_106008C.1

US-10-425-115-6597

Query Match 75.1%; Score 218.6; DB 8; Length 394;

Best Local Similarity 90.3%; Pred. No. 9e-63;

Matches 270; Conservative 0; Mismatches 19; Indels 10; Gaps 3;

Qy 1 AGCCGGCTTTATGCTGCTAGAACTAGTAGCTAGTGGTTGCTGCTGCAATGACACTAT 60

Db 26 AGCCGGCTTTATGCTGCTAGAACTAGTAGCTAGTGGTTGCTGCTGCAATGACACTAT 85

Qy 61 GCAATGTGATCTGGAACCTGGTTCTTGGGTGGCAGCGT-----AGTTATGACTGTC 112

Db 86 GCAATGTGATCTGGAACCTGGTTCTTGGGTGGCAGCGT-----AGTTATGACTGTC 145

Qy 113 GTCAGTAAATTTGGGGCTCCCGTATGAGATGCTGCGGGCAAGGCTCGGTGTCCCA 172

Db 146 GTCGGGAAATTTGGGGCTCCCGTATGAGATGCTGCGGGCAAGGCTCGGTGTCCCA 205

Qy 173 CTTGTTGTGGCGGGGGCGCTGAGCCCGGTCTGGTTGGTTGGGAGGCCCTTTAAAC 232

Db 206 CTTGTTGTGGCGGGGGCGCTGAGCCCGGTCTGGTTGGTTGGGAGGCCCTTTAAAC 264

Qy 233 TGTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTTGTGAGTGGTCTATATCAA 291

Db 265 TGTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTTGTGAGTGGTCTATATCAA 322

#### RESULT 10

US-10-767-701-15432

; Sequence 15432, Application US/10767701

; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 15432

; LENGTH: 1270

; TYPE: DNA

; ORGANISM: Sorghum bicolor

; FEATURE:

; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CJUS49\_330

US-10-767-701-15432

Query Match 74.6%; Score 217; DB 7; Length 1270;

Best Local Similarity 90.0%; Pred. No. 4.8e-62;

Matches 269; Conservative 0; Mismatches 20; Indels 10; Gaps 3;

Qy 1 AGCCGGCTTTATGCTGCTAGAACTAGTAGCTAGTGGTTGCTGCTGCAATGACACTAT 60

Db 890 AGCCGGCTTTATGCTGCTAGAACTAGTAGCTAGTGGTTGCTGCTGCAATGACACTAT 949

Qy 61 GCAATGTGATCTGGAACCTGGTTCTTGGGTGGCAGCGT-----AGTTATGACTGTC 112

Db 950 GCAATGTGATCTGGAACCTGGTTCTTGGGTGGCAGCGT-----AGTTATGACTGTC 1009

Qy 113 GTCAGTAAATTTGGGGCTCCCGTATGAGATGCTGCGGGCAAGGCTCGGTGTCCCA 172

Db 1010 GTCGGGAAATTTGGGGCTCCCGTATGAGATGCTGCGGGCAAGGCTCGGTGTCCCA 1069

Qy 173 CTTGTTGTGGCGGGGGCGCTGAGCCCGGTCTGGTTGGTTGGGAGGCCCTTTAAAC 232

Db 1070 CTTGTTGTGGCGGGGGCGCTGAGCCCGGTCTGGTTGGTTGGGAGGCCCTTTAAAC 1128

Qy 233 TGTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTTGTGAGTGGTCTATATCAA 291

Db 1129 TGTGTGCACTTGCACTTTTACCTTTT-CATCGCTGTTTATTGTGAGTGGTCTTAAATCAA 1186

```

RESULT 11
US-10-425-115-153129
; Sequence 153129, Application US/10425115
; Publication No. US2004021472A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 153129
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577 71235C.1
US-10-425-115-153129

```

Query Match	70.9%	Score 206.2;	DB 8;	Length 464;
Best Local Similarity	86.3%	Pred. No. 1.4e-58;		
Matches 251; Conservative	0;	Mismatches 38;	Indels 2;	Gaps 2;

Qy	1	AGCGCGCTTATGTGC-GTAGAAACTAGTACTAGTCTGTTGCTGCTGCGAATGACACTA	59
Db	173	AGCGCGCTTATGTGCTCTCAAACTAGATGCTAGAGTTTGCTGCTGCGAATGACACTA	232
Qy	60	TGCAATGTGATCTCGAAACCTGGTTTCTTGGGTGCGACGCTAGTTATATGACTGTGCGTCACTA	119
Db	233	TGCAATGCGATCTGCGACCTGCTTCTTGGGCGGCACTCTTGTCTATGACTGTGCACCACTA	292
Qy	120	AAATTTGGGG-GCTCCCGGTATGAGATGCTCCCGGGCAAGGCTCGCGTGTCCCACTCGT	178
Db	293	AAATTTGGGGTGCTCCCGACATGAGATGCTTCCGTACAAGGCCCTCGCTGACCCCACTCGC	352
Qy	179	TTGTGGCGGGGGCGCTGGAGCCCGCTCTGCTTGGGTGGGAAGGCCCTTAAACTGTGTTGT	238
Db	353	TTGAGACGGGGGGCGCTGCACCCGGACTGTGTAGATATGCGAGGCCCTTTAAACTGTGTTGT	412
Qy	239	CACTTGATTTTACCTTTTCATCCGCTGTTTATTTGTGAGTGGTCTCTATATC	289
Db	413	TACTTGAATTTTACCTTTTCATCCGCTGTTTATTTGCGAGGGGCCCTATATC	463

RESULT 12  
 US-10-425-114-15469  
 ; Sequence 15469, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E  
 ; APPLICANT: Tabaska, Jack E  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 15469  
 ; LENGTH: 807  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays

```

; FEATURE:
; - OTHER INFORMATION: Clone ID: LI83060-005-C4_FLI
US-10-425-114-15469

```

Query Match	67.1%;	Score 195.2;	DB 7;	Length 807;
Best Local Similarity	81.5%;	Pred. No. 8.6e-55;		
Matches 243;	Conservative 0;	Mismatches 43;	Indels 12;	Gaps 1;
Qy	1	AGCGGGCTTTATGTGCGGTAGAAACTAGTACTAGTGTTCGTCGTGCGAATGACACTAT	60	
Db	489	AGCGGGCTTTACGTGCGCTTAGAAGCTAGTACTAGTGTTCGTCGTCTAATGACACTAT	548	
Qy	61	GCAATGTGATCTGGAACCTGTTTCTTGGGTCGCACCGCTAGTTATGACTG	110	
Db	549	GCAATGTGATCTGGACCCCTGTTTCTTGGGTCGCACCGCTGTATGATGATT	608	
Qy	111	--TGTCAGTAAATTTGGGGGCTCCCGCTATGAGATGTCGCGGGCAAGCCCTCGGTGT	168	
Db	609	ATTGTGCGGAAATTTGGGGGCTCCCCATATGAGATGTCGCGGGCAAGCCTCGGCAT	668	
Qy	169	CCCACTCTGTTTGTGGCGGGGGCGCTGGAGCCCGGTCTCGTTGGGTTGGGAAGCCCTTT	228	
Db	669	CCCACTCTGTTTCAAGCGGGGGAGCGCTGGAGCGTGGTCCGGTGTGTTGGGAAGCCCTTT	728	
Qy	229	AAACTGTTGCACTTGCAATTTTACCTTTTCCATCGCTGTTTATTTGTGAGTGGTCCCTAT	286	
Db	729	AAACTGTTGCGTGTGATTTTAACTTTTTCATCGCGGTTCAGTGGTCTTAAATCTAT	786	

```

RESULT 3
US-10-425-114-25681
; Sequence 25681, Application US/10425114
; Publication No. US20040034888A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kowalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
;
; TITLE OF INVENTION: Nucleic Acid Molec
;
; TITLE OF INVENTION: Plants and Uses T
;
; FILE REFERENCE: 38-21(53313)B
;
; CURRENT APPLICATION NUMBER: US/10/425,
;
; CURRENT FILING DATE: 2003-04-28
;
; NUMBER OF SEQ ID NOS: 73128
;
; SEQ ID NO 25681
;
; LENGTH: 824
;
; TYPE: DNA
;
; ORGANISM: Zea mays
;
; FEATURE:
;
; OTHER INFORMATION: Clone ID: LIB3957-
US-10-425-114-25681

```

	Query Match	67.1%;	Score 195.2;	DB 7;	Length 824;
	Best Local Similarity	81.5%;	Pred. No. 8.6e-55;		
	Matches 243;	Conservative 0;	Mismatches 43;	Indels 12;	Gaps 1;
QY	1	AGCGCGCTTTATCTGCGGTAGAACTAGTAGTCTAGTGTGTTGCTGCTGTCGAAATGACACTAT	60		
DB	504	AGCGCGCTTTACGTGCTAGACGTAGTACCTAGTGTGTTGCTGCTCTAATGACACTAT	563		
QY	61	GCAATGTGATCTGGAACTCTGGTTCTTTGGGTGGCAAGCTAGTTATGACTG-----	110		
DB	564	GCAATGTGATCTGGACCCCTGGTTTCTTTGGGTGGCAAGCTGTGTAGCAGCCGTGTTATGATTT	623		
QY	111	--TCGTGAGTAAATTTGGGGGCTCCCGGTATCAGATGCTCCGGGCAAGGCGCTCGGTGT	168		
DB	624	ATTGTGCGGAAATTTGGGGGCTCCCCATATAGATGCTCCGGGCGAGACCTCGGCAT	693		
QY	169	CCCACTCGTTTGTGCGGGGGCGCTGGAGCCCGTCTGGTTGGGTGGGAAGCCCTTTT	228		
DB	684	CCCACTCGTTTTCAGCGCGGGAGCGTGGAGCGTGTGCGGTGTGTGTGGGAAGCCCTTT	743		

QY 229 AAACGTGTTGCTACCTGCACTTTTACCTTTTCCATCGCTGTTTATTGAGTGGTCCCTAT 286  
|||||  
Db 744 AAACGTGTTGCTGCTTGCATTTTAACTTTTCACTCCCGTTTCACTGGTCTCTAAATCTAT 801  
|||||

RESULT 14  
US-10-425-114-26656  
; Sequence 26656, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 26656  
; LENGTH: 969  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB4570-004-A10\_FLI  
US-10-425-114-26656

Query Match 67.1%; Score 195.2; DB 7; Length 969;  
Best Local Similarity 81.5%; Pred. No. 9.2e-55;  
Matches 243; Conservative 0; Mismatches 43; Indels 12; Gaps 1;

QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTGTTGCTGTGCTGTCGAATGACACTAT 60  
|||||  
Db 634 AGCCGGCTTTAGTGCCTAGAGCTAGTACCTAGTGTGCTGTCTATGACACTAT 693  
|||||

QY 61 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCTAGTATTGACTG-----110  
|||||  
Db 694 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCTAGTATTGATT 753  
|||||

QY 111 --TCGTCACTAGTAAATTTGGGGCTCCCGTATGATGCTGCCGGCAAGCCCTGTT 168  
|||||  
Db 754 ATTTGTCGGGAAATTTGGGGCTCCCGTATGATGCTGCCGGCAAGCCCTGTT 813  
|||||

QY 169 CCCACCTCGTTTGTGGGGGGCGCTGGAGCCCGTCTGTTGGTGGGAAAGCCCTTT 228  
|||||  
Db 814 CCCACCTCGTTTGTGGGGGGCGCTGGAGCCCGTCTGTTGGTGGGAAAGCCCTTT 873  
|||||

QY 229 AAACGTGTTGCTACCTGCACTTTTACCTTTTCCATCGCTGTTTATTGAGTGGTCCCTAT 286  
|||||  
Db 874 AAACGTGTTGCTGCTTGCATTTTAACTTTTCACTCCCGTTTCACTGGTCTCTAAATCTAT 931  
|||||

RESULT 15  
US-10-425-115-6593  
; Sequence 6593, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 6593  
; LENGTH: 1114

; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_106001C.1  
US-10-425-115-6593

Query Match 67.1%; Score 195.2; DB 8; Length 1114;  
Best Local Similarity 81.5%; Pred. No. 9.6e-55;  
Matches 243; Conservative 0; Mismatches 43; Indels 12; Gaps 1;

QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTGTTTGTGCTGTCGAATGACACTAT 60  
|||||  
Db 634 AGCCGGCTTTACGTGCTAGAACTAGTACCTAGTGTGCTGTCTAATGACACTAT 693  
|||||

QY 61 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCTAGTATTGACTG-----110  
|||||  
Db 694 GCAATGTGATCTGGAACCTGTTTCTTGGGTGCGACGCTAGTATTGATT 753  
|||||

QY 111 --TCGTCACTAGTAAATTTGGGGCTCCCGTATGATGCTGCCGGCAAGCCCTGTT 168  
|||||  
Db 754 ATTTGTCGGGAAATTTGGGGCTCCCGTATGATGCTGCCGGCAAGCCCTGTT 813  
|||||

QY 169 CCCACCTCGTTTGTGGGGGGCGCTGGAGCCCGTCTGTTGGTGGGAAAGCCCTTT 228  
|||||  
Db 814 CCCACCTCGTTTGTGGGGGGCGCTGGAGCCCGTCTGTTGGTGGGAAAGCCCTTT 873  
|||||

QY 229 AAACGTGTTGCTACCTGCACTTTTACCTTTTCCATCGCTGTTTATTGAGTGGTCCCTAT 286  
|||||  
Db 874 AAACGTGTTGCTGCTTGCATTTTAACTTTTCACTCCCGTTTCACTGGTCTCTAAATCTAT 931  
|||||

Search completed: March 8, 2006, 05:20:28  
Job time : 630.177 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 03:46:27 ; Search time 336.308 Seconds  
(without alignments)  
5766.810 Million cell updates/sec

Title: US-10-603-524A-2  
Perfect score: 291  
Sequence: 1 acccgctttatgtcgtag.....tgtgagtggtctatatcaa 291

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_21.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	291	100.0	291	12 ADI22023	ADI22023 Maize 3'
2	285.8	98.2	653	13 ADX36911	Adx36911 Plant ful
3	285.8	98.2	1283	13 ADX46416	Adx46416 Plant ful
4	260.2	89.4	733	13 ADX61388	Adx61388 Plant ful
5	258.2	88.7	689	13 ADX46018	Adx46018 Plant ful
6	253.2	87.0	752	13 ADX61636	Adx61636 Plant ful
7	245.8	84.5	487	13 ADX34364	Adx34364 Plant ful
8	195.2	67.1	807	13 ADX32649	Adx32649 Plant ful
9	195.2	67.1	824	13 ADX50941	Adx50941 Plant ful
10	195.2	67.1	969	13 ADX51916	Adx51916 Plant ful
11	33.8	11.6	76201	12 ADJ62814	ADJ62814 Human ORF
12	33.6	11.5	378	6 ABN79028	ABN79028 Human ORF
13	33.2	11.4	56826	13 ABD33496	ABD33496 Human can
14	32.8	11.3	3879	4 ABL27441	ABL27441 Drosophil
15	32.8	11.3	6613	4 ABL27440	ABL27440 Drosophil
16	32.4	11.1	516	11 ABD17758	ABD17758 Pseudomon
17	32.4	11.1	846	11 ABD17867	ABD17867 Pseudomon
18	32.4	11.1	885	11 ABD17526	ABD17526 Pseudomon
19	32.2	11.1	582	5 ABV56992	ABV56992 Human pro

20	32.2	11.1	1253	11 ACN83015	ACN83015 Breast ca
21	32	11.0	225883	13 ADV34981	ADV34981 Murine CD
22	31.4	10.8	462	5 ABV51301	ABV51301 Human pro
23	31.2	10.7	3372	6 ABK31761	ABK31761 DNA encod
24	31.2	10.7	3492	6 ABQ75954	ABQ75954 Human PPM
25	31.2	10.7	20097	12 ADP47968	ADP47968 Human MRC
26	31.2	10.7	65140	4 AAD17184	AAD17184 Streptomy
27	31.2	10.7	125401	4 AAD17186	AAD17186 Streptomy
28	31	10.7	1650	13 ADT19187	ADT19187 Plant CDN
29	31	10.7	1704	8 ACA25640	ACA25640 Prokaryot
30	31	10.7	1752	8 ACA25826	ACA25826 Prokaryot
31	31	10.7	47686	12 ADQ59461	ADQ59461 Human can
32	31	10.7	47774	14 ADZ13790	ADZ13790 Murine can
33	30.8	10.6	515	6 ABQ44818	ABQ44818 Oligonuel
34	30.8	10.6	515	6 ABQ44819	ABQ44819 Oligonuel
35	30.8	10.6	516	6 ABQ21873	ABQ21873 Oligonuel
36	30.8	10.6	516	6 ABQ21872	ABQ21872 Oligonuel
37	30.8	10.6	531	6 ABQ16314	ABQ16314 Oligonuel
38	30.8	10.6	531	6 ABQ16315	ABQ16315 Oligonuel
39	30.8	10.6	532	6 ABQ50428	ABQ50428 Oligonuel
40	30.8	10.6	532	6 ABQ50429	ABQ50429 Oligonuel
41	30.8	10.6	858	14 ADZ64183	ADZ64183 Human can
42	30.8	10.6	1321	11 ACL32346	ACL32346 Rice abio
43	30.8	10.6	2973	13 ADT20151	ADT20151 Plant CDN
44	30.8	10.6	3898	12 ADQ63136	ADQ63136 Novel hum
45	30.8	10.6	7752	2 AAV38365	AAV38365 Mouse ESX

## ALIGNMENTS

## RESULT 1

ADI22023

ID ADI22023 standard; DNA; 291 BP.

XX AC ADI22023;

XX DT 22-APR-2004 (first entry)

XX DE Maize 3' UTR #2.

XX KW ss; 3' untranslated region; UTR; expression cassette; transformed plant;

XX KW promoter; untranslated leader sequence; genetic engineering.

XX OS Zea mays.

XX PN WO2004003177-A2.

XX PD 08-JAN-2004.

XX PF 25-JUN-2003; 2003WO-US020977.

XX PR 27-JUN-2002; 2002US-0392571P.

XX PA (DOWC ) DOW AGROSCIENCES LLC.

XX PI Cowen NW, Smith KA, Armstrong K;

XX DR WPI; 2004-071986/07.

XX PT New isolated DNA molecule useful for genetic engineering of plants or for

XX PT improving the expression of transgenes in plants, particularly corn

XX PS Claim 1; SEQ ID NO 2; 20pp; English.

XX CC This sequence represents a 3' untranslated region (UTR) which was used in

XX CC the construction of the recombinant expression cassette of the invention.

XX CC The expression cassette is for effecting expression of a foreign gene in

XX CC a transformed plant and comprises a promoter operable in plants, an

XX CC untranslated leader sequence, a foreign gene of interest, and a 3'UTR.

XX CC This cassette may be used to transform plants, for genetic engineering of

XX CC plants or in improving the expression of transgenes in plants.





CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This sequence represents a plant full length insert  
 CC polynucleotide that can be used in the recombinant DNA construct of the  
 CC invention.

SQ Sequence 689 BP; 143 A; 169 C; 195 G; 182 T; 0 U; 0 Other;

Query Match 88.7%; Score 258.2; DB 13; Length 689;  
 Best Local Similarity 94.6%; Pred. No. 8e-75;  
 Matches 281; Conservative 0; Mismatches 8; Indels 8; Gaps 1;

QY 1 AGCGGCTTTATGTGCGTAGAACTAGTAGTGTGCTGTGCTGCGAATGACACTAT 60  
 |||||  
 DB 393 AGCGGCTTTATGTGCGTAGAACTAGTAGTGTGCTGTGCTGCGAATGACACTAT 452  
 |||||

QY 61 GCAATGTGATCTGGAACCTGGTTCTTGGGTGCGACGCT-----AGTTATGACTGTC 112  
 |||||  
 DB 453 GCAATGTGATCTGGAACCTGGTTCTTGGGTGCGACGCTTTGAGCCGTTGATGACTGTC 512  
 |||||

QY 113 GTCAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGGCTCGGTGCCCA 172  
 |||||  
 DB 513 GTCGGTAAATTTGGGGGCTCCCGTAAAGGATGCTGCTGCGCAAGGCTCGGTGCCCA 572  
 |||||

QY 173 CCTGTTGTCGCGGGGCGCTGAGCCGCTGCTGTTGGTGGGAAGCCCTTTAAAC 232  
 |||||  
 DB 573 CCTGTTGTCGCGGGGCGCTGAGCCGCTGCTGTTGGTGGGAAGCCCTTTAAAC 632  
 |||||

QY 233 TGTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTTGAGTGGTCCCTATATC 289  
 |||||  
 DB 633 TGTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTTGAGTGGTCCCTATATC 689  
 |||||

RESULT 6  
 ADX61636  
 ID ADX61636 standard; cDNA; 752 BP.  
 XX  
 AC ADX61636;  
 XX  
 DT 21-APR-2005 (first entry)  
 XX  
 DE Plant full length insert polynucleotide seqid 32479.  
 XX  
 KW plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content; gene; ss.  
 XX  
 OS Unidentified.  
 XX  
 FN US2004034888-A1.  
 XX  
 PD 19-FEB-2004.  
 XX  
 PF 28-APR-2003; 2003US-00425114.  
 XX  
 PR 06-MAY-1999; 99US-00304517.  
 PR 05-NOV-2001; 2001US-00985678.  
 XX  
 PA (LIU/J) LIU J.  
 PA (ZHOU/J) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.  
 PA (TABA/) TABASKA J E.  
 PA (CAO/) CAO Y.  
 XX  
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 XX  
 DR WPI; 2004-180133/17.  
 XX  
 PT New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 XX  
 PS Claim 1; SEQ ID NO 20758; 15pp; English.  
 XX  
 CC The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This sequence represents a plant full length insert  
 CC polynucleotide that can be used in the recombinant DNA construct of the  
 CC invention.

SQ Sequence 689 BP; 143 A; 169 C; 195 G; 182 T; 0 U; 0 Other;

Query Match 88.7%; Score 258.2; DB 13; Length 689;  
 Best Local Similarity 94.6%; Pred. No. 8e-75;  
 Matches 281; Conservative 0; Mismatches 8; Indels 8; Gaps 1;

QY 1 AGCGGCTTTATGTGCGTAGAACTAGTAGTGTGCTGTGCTGCGAATGACACTAT 60  
 |||||  
 DB 393 AGCGGCTTTATGTGCGTAGAACTAGTAGTGTGCTGTGCTGCGAATGACACTAT 452  
 |||||

QY 61 GCAATGTGATCTGGAACCTGGTTCTTGGGTGCGACGCT-----AGTTATGACTGTC 112  
 |||||  
 DB 453 GCAATGTGATCTGGAACCTGGTTCTTGGGTGCGACGCTTTGAGCCGTTGATGACTGTC 512  
 |||||

QY 113 GTCAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCCGGGCAAGGCTCGGTGCCCA 172  
 |||||  
 DB 513 GTCGGTAAATTTGGGGGCTCCCGTAAAGGATGCTGCTGCGCAAGGCTCGGTGCCCA 572  
 |||||

QY 173 CCTGTTGTCGCGGGGCGCTGAGCCGCTGCTGTTGGTGGGAAGCCCTTTAAAC 232  
 |||||  
 DB 573 CCTGTTGTCGCGGGGCGCTGAGCCGCTGCTGTTGGTGGGAAGCCCTTTAAAC 632  
 |||||

QY 233 TGTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTTGAGTGGTCCCTATATC 289  
 |||||  
 DB 633 TGTGTCACTTGCATTTTACCTTTTCCATCGCTGTTTATTTGAGTGGTCCCTATATC 689  
 |||||

RESULT 6  
 ADX61636  
 ID ADX61636 standard; cDNA; 752 BP.  
 XX  
 AC ADX61636;  
 XX  
 DT 21-APR-2005 (first entry)  
 XX  
 DE Plant full length insert polynucleotide seqid 32479.  
 XX  
 KW plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content; gene; ss.  
 XX  
 OS Unidentified.  
 XX  
 FN US2004034888-A1.  
 XX  
 PD 19-FEB-2004.  
 XX  
 PF 28-APR-2003; 2003US-00425114.  
 XX  
 PR 06-MAY-1999; 99US-00304517.  
 PR 05-NOV-2001; 2001US-00985678.  
 XX  
 PA (LIU/J) LIU J.  
 PA (ZHOU/J) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.  
 PA (TABA/) TABASKA J E.  
 PA (CAO/) CAO Y.  
 XX  
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 XX  
 DR WPI; 2004-180133/17.  
 XX  
 PT New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 XX  
 PS Claim 1; SEQ ID NO 20758; 15pp; English.  
 XX  
 CC The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme

PA (TAB//) TABASKA J E.  
 PA (CAOV//) CAO Y.  
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JB, Cao Y;  
 XX WPI; 2004-180133/17.  
 XX  
 XX New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 XX  
 XX Claim 1; SEQ ID NO 32479; 15pp; English.  
 XX  
 XX The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This sequence represents a plant full length insert  
 CC polynucleotide that can be used in the recombinant DNA construct of the  
 CC invention.  
 XX  
 XX Sequence 752 BP; 154 A; 190 C; 210 G; 198 T; 0 U; 0 Other;  
 XX  
 XX Query Match 87.0%; Score 253.2; DB 13; Length 752;  
 XX Best Local Similarity 94.5%; Pred. No. 3.8e-73;  
 XX Matches 276; Conservative 0; Mismatches 8; Indels 8; Gaps 1;  
 XX  
 XX 1 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 60  
 XX 461 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 520  
 XX  
 XX 61 GCAATGTGATCTGGAACCTGTTCTTGGTGGCGACGCT-----AGTTAGACTGTC 112  
 XX 521 GCAATGTGATCTGGAACCTGTTCTTGGTGGCGACGCTTTGAGCGGTGTATGACTGTC 580  
 XX  
 XX 113 GTCAGTAAATTTGGGGCTCCCGTATGAGATGCTGCGGCGAAGGCTCGGTGCCA 172  
 XX 581 GTCCGTAATTTGGGGGCTCCCGTAAAGGATGCTGCTGCGCAAGGCTCGGTGCCA 640  
 XX  
 XX 173 CTCCTGTTGTGGCGGGGCGCTGAGGCCGCTGCTGTTGGTGGGAGCCCTTTAAAC 232  
 XX 641 CCTGCTGTGGCGTGGGGCGCTGAGGCCGCTGCTGTTGGTGGGAGCCCTTTAAAC 700  
 XX  
 XX 233 TGTGTCACCTGCACTTTACCTTTTCCATGCTGTTTATGTGAGTGGTCT 284  
 XX 701 TGTGTCACCTGCACTTTACCTTTTCCATGCTGTTTATGTGAGTGGTCT 752  
 XX  
 XX RESULT 7  
 XX ADX34364  
 XX ID ADX34364 standard; cDNA; 487.BP.  
 XX  
 XX AC ADX34364;  
 XX  
 XX 21-APR-2005 (first entry)  
 XX  
 XX Plant full length insert polynucleotide seqid 17184.  
 XX  
 XX plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

extreme osmotic condition; pathogen tolerance; pest tolerance;  
 growth rate; cell cycle pathway; disease resistance;  
 galactomannan production; lignin production; plant growth regulator;  
 yield; plant growth; plant development; seed oil; protein yield;  
 protein content; gene; ss.  
 Unidentified.  
 US2004034888-A1.  
 19-FEB-2004.  
 28-APR-2003; 2003US-00425114.  
 06-MAY-1999; 99US-00304517.  
 05-NOV-2001; 2001US-00985678.  
 (LIU//) LIU J.  
 (ZHOU//) ZHOU Y.  
 (KOVA//) KOVALIC D K.  
 (SCRE//) SCREEN S E.  
 (TABA//) TABASKA J E.  
 (CAOV//) CAO Y.  
 Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JB, Cao Y;  
 WPI; 2004-180133/17.  
 New recombinant DNA construct, useful for improving plant tolerance to  
 cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 pests, for conferring increased resistance to plant disease, or for  
 improving yield.  
 Claim 1; SEQ ID NO 17184; 15pp; English.  
 The invention describes a recombinant DNA construct comprising a  
 polynucleotide consisting of a sequence encoding an amino acid sequence  
 available in electronic form from the US patent office at  
 ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
 of the invention are also useful in physical arrays of molecules and as  
 plant breeding markers. The recombinant DNA construct is useful for  
 improving plant tolerance to cold, heat, drought, herbicides, extreme  
 osmotic conditions, pathogens or pests, for manipulating growth rate in  
 plant cells by modification of the cell cycle pathway, for conferring  
 increased resistance to plant disease, for producing galactomannan,  
 lignin or plant growth regulators, for increasing the rate of homologous  
 recombination in plants, for improving yield by modification of  
 photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 or by providing improved plant growth and development under at least one  
 stress condition or for modifying seed oil or protein yield and/or  
 content. This sequence represents a plant full length insert  
 polynucleotide that can be used in the recombinant DNA construct of the  
 invention.  
 Sequence 487 BP; 99 A; 118 C; 143 G; 127 T; 0 U; 0 Other;  
 Query Match 84.5%; Score 245.8; DB 13; Length 487;  
 Best Local Similarity 99.2%; Pred. No. 8.8e-71;  
 Matches 247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 60  
 239 AGCCGGCTTTATGTGCGTAGAACTAGTAGCTAGTGTGCTGTGCTGCGAATGACACTAT 298  
 61 GCAATGTGATCTGGAACCTGTTCTTGGTGGCGACGCTTTGTTAGTACTGTCGTCAGTAA 120  
 299 GCAATGTGATCTGGAACCTGTTCTTGGTGGCGACGCTTTGTTAGTACTGTCGTCAGTAA 358  
 121 AATTGGGGGCTCCCGTATGAGATGCTGCGGCGAAGGCTCGGTGCCACCTCGTTT 180  
 359 AATTGGGGGCTCCCGTATGAGATGCTGCGGCGAAGGCTCGGTGCCACCTCGTTT 418  
 181 GTGGCGGGGGCGCTGGAGCCCGGTCTGTTGGTGGGAGCCCTTTAAACTGTTGTCA 240

Db 419 GTGGCGGGGGCTGGAGCCCGTCTGGTGGGTTGGGAAGCCCTTTAAACTGTGTGCA 478  
QY 241 CTTGCATTT 249  
Db 479 CTTGCATTT 487  
RESULT 8  
ADX32649  
ID ADX32649 standard; cDNA; 807 BP.  
XX  
AC ADX32649;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polynucleotide seqid 15469.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
OS Unidentified.  
XX  
PN US2004034888-A1.  
XX  
PD 19-FEB-2004.  
XX  
PF 28-APR-2003; 2003US-00425114.  
XX  
PR 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX  
DR WPI; 2004-180133/17.  
XX  
PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
PS Claim 1; SEQ ID NO 15469; 15pp; English.  
XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the

CC invention.  
XX  
SQ Sequence 807 BP; 172 A; 213 C; 214 G; 208 T; 0 U; 0 Other;  
Query Match 67.1%; Score 195.2; DB 13; Length 807;  
Best Local Similarity 81.5%; Pred. No. 6.2e-54;  
Matches 243; Conservative 0; Mismatches 43; Indels 12; Gaps 1;  
QY 1 AGCGGCTTTATGTGCTAGAACTAGTAGCTAGTGTGCTGCTGGAATGACACTAT 60  
Db 489 AGCCGGCTTTACGTGCTAGAGCTAGTACCTAGTGTGCTGCTGCTATGACACTAT 548  
QY 61 GCAATGTGATCTGGAACCTGCTTTCTTGGGTGCGACGCTAGTATGACTG----- 110  
Db 549 GCAATGTGATCTGGAACCTGCTTTCTTGGGTGCGACGCTGCTAGCAGCGCTGTTATGATT 608  
QY 111 --TCGTGAGTAAATTTGGGGGCTCCCGTATGATGCTCCCGGCGAAGCCCTCGGTGT 168  
Db 609 ATTTGTGCGGAAATTTGGGGGCTCCCATATGATGCTCCCGGCGAAGCCCTCGGCAT 668  
QY 169 CCCACCTCGTTTGGCGGGGGGCTGGAGCCCGCTGCTGCTGGTTGGGAAGCCCTTT 228  
Db 669 CCCACCTCGTTTTCAGGCGGGGACGCTGGAGCGTGGTCCGGTTGTGTGGGAAGCCCTT 728  
QY 229 AAACCTGTGTGACATTTTACCTTTTCCATCGCTGTTTATTTGAGTGGTCTCTAT 286  
Db 729 AAACCTGTGTGCTTGCATTTTAACTTTTTCATCGCGCTTCAGTGGTCTCTAAATCTAT 786  
RESULT 9  
ADX50941  
ID ADX50941 standard; cDNA; 824 BP.  
XX  
AC ADX50941;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polynucleotide seqid 25681.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
OS Unidentified.  
XX  
PN US2004034888-A1.  
XX  
PD 19-FEB-2004.  
XX  
PF 28-APR-2003; 2003US-00425114.  
XX  
PR 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX  
DR WPI; 2004-180133/17.  
XX  
PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for

```
PT improving yield.
XX
PS Claim 1; SEQ ID NO 25681; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 824 BP; 178 A; 216 C; 218 G; 212 T; 0 U; 0 Other;
XX
Query Match 67.1%; Score 195.2; DB 13; Length 824;
Best Local Similarity 81.5%; Pred. No. 6.3e-54;
Matches 243; Conservative 0; Mismatches 43; Indels 12; Gaps 1;
XX
QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGTGTGTTGCTGCTGCGAATGACACTAT 60
DB 504 AGCCGGCTTTATGTCGTAGAACTAGTAGTGTGTTGCTGCTGCGAATGACACTAT 563
QY 61 GCAATGTGATCTGGAACTGCTGTTCTTGGGTGCGACGCTAGTATGACTG 110
DB 564 GCAATGTGATCTGGAACTGCTGTTCTTGGGTGCGACGCTAGTATGACTG 623
QY 111 --TCGTAGTAAATTTGGGGGCTCCCGTATGAGATGTCGCGGCAAGCGCTCGGTGT 168
DB 624 ATTTCGCGGAAATTTGGGGGCTCCCGTATGAGATGTCGCGGCAAGCGCTCGGTGT 683
QY 169 CCACCTCGTTGTCGCGGGGGCGCTGAGCCGCTGCTGTTGGTGGGAGCCCTTT 228
DB 684 CCACCTCGTTGTCGCGGGGGCGCTGAGCCGCTGCTGTTGGTGGGAGCCCTTT 743
QY 229 AAACCTGTTGTCACCTGTCATTTTACCTTTTCCATCGCTGTTTATGAGTGTCTAT 286
DB 744 AAACCTGTTGTCGTTGTCATTTTAACTTTTTCATCGCGCTTCACTGCTCTAATCTAT 801
XX
RESULT 10
ID ADX51916 standard; cDNA; 969 BP.
XX
AC ADX51916;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 26656.
XX
KW plant protectant; plant growth regulator; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
FN US2004034888-A1.
XX
```

```
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIU/J) LIU J.
PA (ZHOU/Y) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABR/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
WPI; 2004-180133/17.
XX
DR New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 26656; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 969 BP; 218 A; 238 C; 269 G; 244 T; 0 U; 0 Other;
XX
Query Match 67.1%; Score 195.2; DB 13; Length 969;
Best Local Similarity 81.5%; Pred. No. 6.7e-54;
Matches 243; Conservative 0; Mismatches 43; Indels 12; Gaps 1;
XX
QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGTGTGTTGCTGCTGCGAATGACACTAT 60
DB 634 AGCCGGCTTTATGTCGTAGAACTAGTAGTGTGTTGCTGCTGCGAATGACACTAT 693
QY 61 GCAATGTGATCTGGAACTGCTGTTCTTGGGTGCGACGCTAGTATGACTG 110
DB 694 GCAATGTGATCTGGAACTGCTGTTCTTGGGTGCGACGCTAGTATGACTG 753
QY 111 --TCGTAGTAAATTTGGGGGCTCCCGTATGAGATGTCGCGGCAAGCGCTCGGTGT 168
DB 754 ATTTCGCGGAAATTTGGGGGCTCCCGTATGAGATGTCGCGGCAAGCGCTCGGTGT 813
QY 169 CCCACCTCGTTGTCGCGGGGGCGCTGAGCCGCTGCTGTTGGTGGGAGCCCTTT 228
DB 814 CCCACCTCGTTGTCGCGGGGGCGCTGAGCCGCTGCTGTTGGTGGGAGCCCTTT 873
QY 229 AAACCTGTTGTCACCTGTCATTTTACCTTTTCCATCGCTGTTTATGAGTGTCTAT 286
DB 874 AAACCTGTTGTCGTTGTCATTTTAACTTTTTCATCGCGCTTCACTGCTCTAATCTAT 931
XX
RESULT 11
ADJ62814/c
```

ID ADJ62814 standard; cDNA; 76201 BP.  
 AC ADJ62814;  
 XX  
 DT 06-MAY-2004 (first entry)  
 DE Human cDNA differentially expressed in response to docetaxel #84.  
 KW array; docetaxel; docetaxel resistance; cancer; human; ss;  
 KW differential expression.  
 XX Homo sapiens.  
 OS  
 PN US2004018527-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 16-MAY-2003; 2003US-00439703.  
 XX  
 PR 17-MAY-2002; 2002US-0381141P.  
 XX  
 PA (CHAN/) CHANG J C.  
 PA (OCON/) O'CONNELL P.  
 XX  
 PI Chang JC, O'connell P;  
 XX  
 DR WPI; 2004-224389/21.  
 XX  
 PT Array useful for screening patient for resistance to docetaxel comprises  
 PT complementary nucleic acid probes attached to solid surface.  
 XX  
 PS Claim 21; SEQ ID NO 84; 169pp; English.  
 XX  
 CC The invention relates to an array for screening a patient for resistance  
 CC to docetaxel comprising complementary nucleic acid probes attached to a  
 CC solid surface for at least 10 of the nucleic acids chosen from 91 fully  
 CC defined sequences as given in the specification. The array is useful for  
 CC screening a patient for resistance to docetaxel. The array is also useful  
 CC for monitoring a cancer patient receiving docetaxel therapy. The present  
 CC sequence represents a human cDNA differentially expressed in response to  
 CC docetaxel.  
 XX  
 SQ Sequence 76201 BP; 19685 A; 17309 C; 18629 G; 20578 T; 0 U; 0 Other;  
 Query Match 11.6%; Score 33.8; DB 12; Length 76201;  
 Best Local Similarity 64.9%; Pred. No. 12;  
 Matches 50; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
 QY 147 CTGCGGGCAAGGCTCGGTGTCACCTGCTTGTGGGGGGGGCGTGGAGCCCGTTC 206  
 Db 12996 CGGCGGGGATTCGCTTCGTGTCCTCCCTGCGGGGGGGAGTGGGGGGCGGGCG 12937  
 QY 207 TGGTTGGGTTGGGAAGC 223  
 Db 12936 TGGGAGGTTTGAAGAAGC 12920  
 RESULT 12  
 ABN79028/c  
 ID ABN79028 standard; cDNA; 378 BP.  
 XX  
 AC ABN79028;  
 XX  
 DT 08-JUL-2002 (first entry)  
 DE Human ORF3975 cDNA, SEQ ID NO:7949.  
 XX  
 KW Human; ORF; open reading frame; ORFX; drug screening; diagnosis;  
 KW disease monitoring; cytokine; cell proliferation; cell differentiation;  
 KW immune modulation; haematopoiesis regulation; tissue growth;  
 KW angiogenesis; activin; inhibitor; chemotactic; chemokinetic; haemostatic;  
 KW thrombolytic; tumour inhibition; bodily characteristic; fertility;  
 KW behaviour; cancer; proliferative disorder; neurological disorder;

KW cardiovascular disease; immune system disorder; organ transplantation;  
 KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;  
 KW hypothyroidism; cholesterol ester storage disease; infection; vulnary;  
 KW vasotropic; antipsoriatic; antidiabetic; cycostatic; nootropic;  
 KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;  
 KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;  
 KW dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.  
 XX Homo sapiens.  
 OS  
 PN WO200190366-A2.  
 XX  
 PD 29-NOV-2001.  
 XX  
 PF 24-MAY-2001; 2001WO-US017076.  
 XX  
 PR 24-MAY-2000; 2000US-0206690P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Leach MD, Shimkets RA;  
 XX  
 DR WPI; 2002-106200/14.  
 DR P-PSDB; ABP35002.  
 XX  
 PT Novel human polypeptides and polynucleotides useful for diagnosing,  
 PT preventing and treating cardiovascular disease, neurodegenerative,  
 PT hyperproliferative disorders and disorders related to organ  
 PT transplantation.  
 XX  
 PS Claim 1; Page 2233; 2508pp; English.  
 XX  
 CC Sequences ABP31028-ABP35561 represent 4534 novel human proteins  
 CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-  
 CC ABN79587 represent cDNAs encoding them. The invention also encompasses  
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively  
 CC referred to as ORFX) proteins, polynucleotides at least 85% identical to  
 CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX  
 CC polynucleotides, the recombinant production of ORFX proteins, antibodies  
 CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and  
 CC polypeptides, methods of screening for modulators of ORFX expression or  
 CC activity, and methods of screening individuals for a predisposition to an  
 CC ORFX-associated disorder. The ORFX proteins of the invention have a wide  
 CC range of biological activities, such as cytokine, cell proliferation,  
 CC cell differentiation, immune modulation, haematopoiesis regulation,  
 CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/  
 CC chemokinetic activity, haemostatic activity, thrombolytic activity,  
 CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,  
 CC and antiinfective activity, and may also be involved in the determination  
 CC of bodily characteristics, fertility and behaviour. ORFX proteins,  
 CC nucleic acids and antibodies may be used in the treatment of cancers,  
 CC other proliferative disorders such as psoriasis and benign tumours,  
 CC neurological disorders such as epilepsy and Alzheimer's disease,  
 CC cardiovascular diseases, immune system disorders, disorders related to  
 CC organ transplantation, disorders of tissue growth and regeneration,  
 CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester  
 CC storage disease, and infectious diseases caused by viral, bacterial,  
 CC fungal and other pathogens. ORFX nucleic acids may also be used as a  
 CC source of primers and probes, in the detection of ORFX genomic sequences  
 CC or transcripts, in the identification and cloning of homologous  
 CC sequences, in genetic diagnosis, and in forensic biology. The ORFX  
 CC nucleic acids may additionally be used to produce transgenic animals  
 CC which may be useful for studying the function and/or activity of ORFX  
 CC protein, and in drug screening. The ORFX proteins may also be used as  
 CC immunogens to generate specific antibodies, which are useful in the  
 CC diagnosis, treatment and monitoring of ORFX-associated diseases  
 XX  
 SQ Sequence 378 BP; 61 A; 122 C; 150 G; 42 T; 0 U; 3 Other;  
 Query Match 11.5%; Score 33.6; DB 6; Length 378;  
 Best Local Similarity 53.5%; Pred. No. 1.5;  
 Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;







GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 03:57:42 ; Search time 2087.91 Seconds  
(without alignments)  
7922.477 Million cell updates/sec

Title: US-10-603-524A-2

Perfect score: 291

Sequence: 1 agcggctttatgtcgtag.....tgtgagtggtctatatca 291

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.in.\*

3: gb.env.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pr.\*

9: gb.ro.\*

10: gb.sts.\*

11: gb.ev.\*

12: gb.un.\*

13: gb.vi.\*

14: gb.htg.\*

15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	260.2	89.4	1189	15 BT017754	BT017754 Zea mays
2	259.8	89.3	320	10 G71239	G71239 716223731FM
3	258.6	88.9	5348	15 S71133	S71133 GRF1-genera
4	220.2	75.7	372	10 G70551	G70551 716223731FB
5	195.2	67.1	1194	15 BT016497	BT016497 Zea mays
6	183.2	63.0	1082	15 MZERE6P	MZERE6P Zea mays re
7	144.8	49.8	327	10 BV150852	BV150852 PZA02088-
8	144.8	49.8	338	10 BV150853	BV150853 PZA02088-
9	144.8	49.8	338	10 BV150856	BV150856 PZA02088-
10	144.8	49.8	338	10 BV150858	BV150858 PZA02088-
11	144.8	49.8	338	10 BV150859	BV150859 PZA02088-
12	144.8	49.8	338	10 BV150861	BV150861 PZA02088-
13	144.8	49.8	338	10 BV150863	BV150863 PZA02088-
14	143.8	49.4	325	10 BV150862	BV150862 PZA02088-
15	143.8	49.4	327	10 BV150860	BV150860 PZA02088-
16	139.2	47.8	324	10 BV150855	BV150855 PZA02088-
17	132.8	45.6	334	10 BV150854	BV150854 PZA02088-
18	132.4	45.5	290	10 BV150857	BV150857 PZA02088-

19	38	13.1	205310	14	AC125979
20	38	13.1	229726	14	AC109699
c 21	37.6	12.9	140505	14	AC150176
22	36.8	12.6	82806	8	AC007111
23	36.8	12.6	183396	14	AC154112
24	36.8	12.6	196413	14	AC097269
25	36.8	12.6	199759	8	AC009065
26	36.8	12.6	239434	14	AC012171
27	36.6	12.6	185573	14	AC010994
c 28	36.2	12.4	300349	1	AE017319
29	36	12.4	110000	15	CR380957
c 30	35.4	12.2	187350	8	AC020713
c 31	35	12.0	12973	14	AC013026
32	35	12.0	170914	2	AC010843
33	35	12.0	296756	2	AE003492
c 34	34.6	11.9	842	6	CQ714812
c 35	34.6	11.9	1465	8	HSU48224
c 36	34.6	11.9	150788	14	AF087130
c 37	34.6	11.9	167662	8	AC055753
c 38	34.6	11.9	172697	14	AC076965
c 39	34.6	11.8	169547	9	AL590503
c 40	34.2	11.8	200830	9	AC153845
41	34.2	11.8	207347	14	AC109628
42	34.2	11.8	230492	14	AC159467
c 43	34	11.7	257916	14	AC095894
44	34	11.7	293405	14	AC128473
c 45	34	11.7	293405	14	AC128473

#### ALIGNMENTS

#### RESULT 1

BT017754/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BT017754 1189 bp mRNA linear PLN 27-OCT-2004  
Zea mays clone EL01N0450F06.c mRNA sequence.

BT017754

BT017754.1 GI:54652535

BT017754.1

FLI CDNA.

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1189)

Lai, J., Dey, N., Kim, C.-S., Bharti, A.K., Rudd, S., Mayer, K.F.X.,

Larkins, B., Becraft, P. and Messing, J.

Characterization of the maize endosperm transcriptome and its

comparison to the rice genome

Unpublished

2 (bases 1 to 1189)

Lai, J., Dey, N., Kim, C.-S., Bharti, A.K., Rudd, S., Mayer, K.F.X.,

Larkins, B., Becraft, P. and Messing, J.

Direct Submission

Submitted (27-OCT-2004) Waksman Institute, Rutgers University, 190

Frelinghuysen Rd, Piscataway, NJ 08854, USA

Location/Qualifiers

1..1189

/organism="Zea mays"

/mol\_type="mRNA"

/db\_xref="taxon:4577"

/clone="EL01N0450F06.c"

Query Match 89.4%; Score 260.2; DB 15; Length 1189;

Best Local Similarity 94.6%; Pred. No. 9.5e-61;

Matches 283; Conservative. 0; Mismatches 8; Indels 8; Gaps 1;

Qy 1 AGCGCGCTTTATGTCGTAGAACTAGTAGCTGTTGCTGCTGCAATGACACTAT 60

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Db 311 AGCGCGCTTTATGTCGTAGAACTAGTAGCTGTTGCTGCTGCAATGACACTAT 252

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Qy 61 GCAATGTGATCTGGAACCTGTTTCTTTGGTGCACGCT-----AGTTATGACTGTC 112

Db 251 GCAATGTGATCTGGAACCTGGTTCTTGGGTGCGAGCGCTTGAGCCGGTTATGACTGTC 192  
Qy 113 GTCAGTAAATTTGGGGGCTCCCGTATGAGATGCTGCGGCAAGGCTCGGTGTCCA 172  
Db 191 GTCGTAATTTGGGGGCTCCCGTAAAGGATGCTGCTGGCAAGGCTCGGTGTCCA 132  
Qy 173 CCTCGTTTGTGGCGGGGCGCTGGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAAC 232  
Db 131 CCTGCTGTGGGCTGGGGCGCTGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAAAC 72  
Qy 233 TGTGTGCACTTGCAATTTTACCTTTTCCATCGCTGTTTATTTGAGTGGTCTCTATATCAA 291  
Db 71 TGTGTGCACTTGCAATTTTACCTTTTCCATCGCTGTTTATTTGAGTGGTCTCTATATCAA 13

RESULT 2  
G71239  
LOCUS 716223731FWo17 maize leaf DNA Zea mays STS 08-JUN-2001  
DEFINITION 320 bp DNA linear STS genomic, sequence tagged  
ACCESSION G71239  
VERSION G71239.1 GI:14332924  
KEYWORDS STS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 320)  
AUTHORS Yang, Y.J., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.  
TITLE 3' UTR sequences of maize genes  
JOURNAL Unpublished (2001)  
COMMENT

Contact: Schnable, P.S.  
Schnable laboratory  
Iowa State University  
G405 Agronomy Hall, Ames, IA 50011, USA  
Tel: 515-294-0975  
Fax: 515-294-2299  
Email: schnable@iastate.edu  
Primer A: GAGCGAGGAGTCTTACAAAG  
Primer B: GCGATGGAAGGTAATAATGC  
PCR Profile:  
Denaturation: 94 degrees C for 30 seconds  
Annealing: 60 degrees C for 45 seconds  
Polymerization: 72 degrees C for 90 seconds  
PCR cycles: 31  
Thermal cycler: Perkin Elmer TC  
Protocol:  
Template: 10-20 ng  
Primer: each 0.5 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/uL  
Total vol: 20 uL

Buffer:  
MgCl2: 2 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.4.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
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/db\_xref="taxon:4577"  
/clone\_lib="maize leaf DNA"  
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STs  
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Query Match 89.3%; Score 259.8; DB 10; Length 320;  
Best Local Similarity 94.3%; Pred. No. 2.6e-60;  
Matches 282; Conservative 0; Mismatches 9; Indels 8; Gaps 1;

Best Local Similarity 99.2%; Pred. No. 1.2e-60;  
Matches 261; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 AGCCGGCTTTATGTCGTAGAACTAGTAGTCTGTTGCTGCTGCAATGACACTAT 60  
Db 58 AGCCGGCTTTATGTCGTAGAACTAGTAGTCTGTTGCTGCTGCAATGACACTAT 117  
Qy 61 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTATGATGCTGTCAGTAA 120  
Db 118 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTTGTATGACTGTCGTCAGTAA 177  
Qy 121 AATTGGGGGCTCCCCGCTATGAGATGCTGCGGCAAGGCTCGGTGTCACCTCGTTT 180  
Db 178 AATTGGGGGCTCCCCGCTATGAGATGCTGCGGCAAGGCTCGGTGTCACCTCGTTT 237  
Qy 181 GTGGCGGGGCGCTCGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAACTGTTGTCA 240  
Db 238 GTGGCGGGGCGCTCGAGCCCGGTCTGGTTGGGTGGGAAGCCCTTTAACTGTTGTCA 297  
Qy 241 CTTCGATTTTACCTTTTCCATCG 263  
Db 298 CTTCGATTTTACCTTTTCCATCG 320

RESULT 3  
S77133  
LOCUS S77133 5348 bp DNA linear PLN 26-SEP-1995  
DEFINITION GRF1=general regulatory factor [Zea mays, XL80, Genomic, 5348 nt].  
ACCESSION S77133  
VERSION S77133.1 GI:998429  
KEYWORDS Zea mays  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 5348)  
AUTHORS de Vetten, N.C. and Perl, R.J.  
TITLE Two genes encoding GF14 (14-3-3) proteins in Zea mays. Structure,  
expression, and potential regulation by the G-box binding complex  
Plant Physiol. 106 (4), 1593-1604 (1994)  
7846163  
REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbs 164519] from the original journal article.

FEATURES  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:4577"  
mRNA join(1491..2583,2671..2749,2876..2998,4387..4503,  
4610..4968)  
2177..4669  
gene /gene="GRF1"  
/note="general regulatory factor"  
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4610..4669)  
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/db\_xref="GI:998430"  
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VEENLLSVAYKNVIGARRASWRIISIEQKEGREGNEDVTLLKDYRGKIELTKI  
CDGILKLETHLPSTAPESKVFYLMKGDYVYLAERFTGAERKDAENTVMYAKA  
AQDIALAELAPTHPIRLGLALNFSVFYELNSPDRACSLAKQAFDEAISLDTLSE  
SYKDSITLMQLLRDNLTLWTSDISDPAEIREAPKDSSEGG"  
ORIGIN

Query Match 88.9%; Score 258.6; DB 15; Length 5348;  
Best Local Similarity 94.3%; Pred. No. 2.6e-60;  
Matches 282; Conservative 0; Mismatches 9; Indels 8; Gaps 1;

QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGCTGCTGCAATGACACTAT 60  
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 Db 4670 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGCTGCTGCAATGACACTAT 4729  
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 QY 61 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCT-----AGTTATGACTGTC 112  
 |||||  
 Db 4730 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTTGAACCGTGTATGACTGTC 4789  
 |||||  
 QY 113 GTCAGTAAATTTGGGGGCTCCCGGTATGAGATGCTGCGGGCAAGGCTCGGTGTCCA 172  
 |||||  
 Db 4790 GTCCGTAATTTGGGGGCTCCCGTAAGGATGCTGCTGCGCAAGGCTCGGTGTCCA 4849  
 |||||  
 QY 173 CCTGTTTGTGGGGGCGCTGGAGCCGCTGTTGGTGGGAGCCCTTTAAAC 232  
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 Db 4850 CCTGTTTGTGGGGGCGCTGGAGCCGCTGTTGGTGGGAGCCCTTTAAAC 4909  
 |||||  
 QY 233 TGTGTGCTGCAATTTTACCTTTTCCATCGCTGTTTATGAGTGGTGCCTATATCAA 291  
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 Db 4910 TGTGTGCTGCAATTTTACCTTTTCCATCGCTGTTTATGAGTGGTGCCTATATCAA 4968  
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RESULT 4  
 G70551  
 LOCUS 716223731PB73 maize leaf DNA Zea mays STS 08-JUN-2001  
 DEFINITION site.  
 ACCESSION G70551  
 VERSION G70551.1 GI:14332236  
 KEYWORDS STS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 372)  
 AUTHORS Yang, Y.J., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.  
 TITLE 3' UTR sequences of maize genes  
 JOURNAL Unpublished (2001)  
 COMMENT

Contact: Schnable, P.S.  
 Schnable laboratory  
 Iowa State University  
 4405 Agronomy Hall, Ames, IA 50011, USA  
 Tel: 515-294-0975  
 Fax: 515-294-2299  
 Email: schnable@iastate.edu  
 Primer A: GAGCGAGGAGTCTTACCAAGG  
 Primer B: GCGATGGAAAGGTAAATGC  
 PCR Profile:  
 Denaturation: 94 degrees C for 30 seconds  
 Annealing: 60 degrees C for 45 seconds  
 Polymerization: 72 degrees C for 90 seconds  
 PCR cycles: 31  
 Thermal cycler: Perkin Elmer TC  
 Protocol:  
 Template: 10-20 ng  
 Primer: each 0.5 uM  
 dNTPs: each 200 uM  
 Taq Polymerase: 0.05 units/ul  
 Total vol: 20 ul

Buffer:  
 MgCl2: 2 mM  
 KCl: 50 mM  
 Tris-HCl: 20 mM  
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FEATURES  
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STS  
 ORIGIN  
 /note="PCR products amplified from genomic DNA"  
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 Db 114 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGCTGCAATGACACTAT 173  
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 QY 61 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCT-----AGTTATGACTGTC 112  
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 Db 174 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTTGTAGCCGCTTATGACTGTC 233  
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 QY 113 GTCAGTAAATTTGGGGGCTCCCGGTATGAGATGCTGCGGGCAAGGCTCGGTGTCCA 172  
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 Db 234 GTCAGTAAATTTGGGGGCTCCCGTAAGGATGCTGCTGCGCAAGGCTCGGTGTCCA 293  
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 QY 173 CCTGTTTGTGGGGGCGCTGGAGCCGCTGTTGGTGGGAGCCCTTTAAAC 232  
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 Db 294 CCTGTTTGTGGGGGCGCTGGAGCCGCTGTTGGTGGGAGCCCTTTAAAC 353  
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 QY 233 TGTGTGCTGCAATTTTACCTTTTCCATCGCTGTTTATGAGTGGTGCCTATATCAA 251  
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 Db 354 TGTGTGCTGCAATTTTACCTTTTCCATCGCTGTTTATGAGTGGTGCCTATATCAA 372  
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RESULT 5  
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 DEFINITION Zea mays clone Contig330 mRNA sequence.  
 ACCESSION BT016497  
 VERSION BT016497.1 GI:54651278  
 KEYWORDS FLI\_CDNA.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 1194)  
 AUTHORS Lai, J., Dey, N., Kim, C.-S., Bharti, A.K., Rudd, S., Mayer, K.F.X.,  
 Larkins, B., Becraft, P. and Messing, J.  
 TITLE Characterization of the maize endosperm transcriptome and its  
 comparison to the rice genome  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1194)  
 AUTHORS Lai, J., Dey, N., Kim, C.-S., Bharti, A.K., Rudd, S., Mayer, K.F.X.,  
 Larkins, B., Becraft, P. and Messing, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-OCT-2004) Waksman Institute, Rutgers University, 190  
 Frelinghuysen Rd, Piscataway, NJ 08854, USA  
 FEATURES  
 Location/Qualifiers  
 1..1194  
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ORIGIN

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 QY 1 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGCTGCAATGACACTAT 60  
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 Db 857 AGCCGGCTTTATGTCGTAGAACTAGTAGCTAGTGTGCTGCTGCAATGACACTAT 916  
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 QY 61 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTAGTATGACTGCT----- 111  
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 Db 917 GCAATGTGATCTGGAACCTGGTTTCTTGGGTGCGACGCTTGTAGCACCAGCTGTTATGATT 976  
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QY	167	GTCCACACCTCGTTTGGCGGGGGCGCTGGAGCCCGGCTCTGCTTGGTTGGGAAGCCCT	226
Db	941	CCCCACACCTCGTTTCAGGCGGGGACCGCTGGAGCCTGGTCCGGTTCGGTTGGGAAGCCCC	1000
QY	227	TTAAACGTGTGCACCTTGTCATTTTACCTTTTCATCGCTGTTTATTGTGAGTGGTCTCTAT	286
Db	1001	TTAAACGTGTGCGCTTGTCATTTTAAACCTTTTCATCGCGGTCAGTGGTCCCTAAATCTAT	1060
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LOCUS	BV150852		
DEFINITION	PZA02088-74466-B73	Zea mays B73	DNA linear STS 11-MAY-2004
ACCESSION	BV150852		
VERSION	BV150852.1	GI:47100309	
KEYWORDS	STS.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	McMullen,M.D., Vrieh Bi,I., Schultz,L., Duru,N., Schroeder,S.S., Sanchez-Villeda,H., Houchins,K., Fang,Z., Polacco,M., Gardiner,J. and Coe,E.H.Jr.		
TITLE	MWP SNP Discovery		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Michael D. McMullen Maize Mapping Project University of Missouri-Columbia 101 Curtis Hall, Columbia, MO 65211-7020, USA		

301 Curciss Hall, Columbia, MO 65211-7020, USA  
Tel: 5738827606  
Fax: 5738847850  
Email: McMullenM@missouri.edu  
Primer A: CTATGCAATGTGATCTGGAACTTG  
Primer B: TAAGATGGGATGGGACACGACAAAT  
Protocol:  
PCR amplification of genomic DNA  
Template: 50 ng  
Primer: each 0.5 uM  
dNTPs: each 200 uM  
Taq Polymerase: RedTaq (Sigma)  
Total Vol: 10 ul  
Amplicon sequencing  
ABI protocol - using d-Rhodamine terminator cycle  
sequencing ready reaction with ampliTaq DNA polymerase FS  
Sequence ran on ABI 3700 sequencer.  
  
Buffer:  
Genomic DNA amplification  
RedTaq (Sigma)  
Sequencing buffer  
d-Rhodamine kit (ABI)

[illegible]

U. Location/Qualifiers

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1. .327
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/mol_type="genomic DNA"
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/clone_lib="Zea mays B73"
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/note="Organ: leaf; genomic DNA from inbred line"
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STS
ORIGIN
Query Match 49.8%; Score 144.8; DB 10; Length 327;
Best Local Similarity 79.4%; Pred. No. 5.6e-29;
Matches 189; Conservative 0; Mismatches 37; Indels 12; Gaps 1;

QY 61 GCAATGTGATCTGGAACCTGTTCTTGGTGCGACGCTAGTATGACTGTC----- 112
Db 1 GCAATGTGATCTGGAACCTGTTCTTGGTGCGACGCTAGTATGACTGTTATGATT 60
QY 113 ----GTCACTAAATTTGGGGCTCCCGTATGAGATGCTCGCGGCAAGCGCTCGGTGT 168
Db 1 GCAATGTGATCTGGAACCTGTTCTTGGTGCGACGCTAGTATGACTGTC----- 112
QY 169 CCCACTGTTGTGGCGGGGCGCTCGAGCCGCTGCTGTTGTTGAGTGGTCCCTAT 228
Db 1 ATTTGTCGGGAAAATTTGGGGCTCCCATATGAGATGCTCGCGGCAAGCGCTCGGCAT 120
QY 229 AAACCTGTTGCTCACTTTCATTTTACCTTTTCCATGCTGTTTATGAGTGGTCCCTAT 286
Db 181 AAACCTGTTGCTGCTTTCATTTTAACTTTTTCATGCGGCTGAGTGGTCTTAATCTAT 238

FEATURES
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/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="CO159"
/db_xref="taxon:4577"
/clone_lib="Zea mays CO159"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
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STS
ORIGIN
Query Match 49.8%; Score 144.8; DB 10; Length 338;
Best Local Similarity 79.4%; Pred. No. 5.6e-29;
Matches 189; Conservative 0; Mismatches 37; Indels 12; Gaps 1;

QY 61 GCAATGTGATCTGGAACCTGTTCTTGGTGCGACGCTAGTATGACTGTC----- 112
Db 1 GCAATGTGATCTGGAACCTGTTCTTGGTGCGACGCTAGTATGACTGTTATGATT 60
QY 113 ----GTCACTAAATTTGGGGCTCCCGTATGAGATGCTCGCGGCAAGCGCTCGGTGT 168
Db 1 ATTTGTCGGGAAAATTTGGGGCTCCCATATGAGATGCTCGCGGCAAGCGCTCGGCAT 120
QY 169 CCCACTGTTGTGGCGGGGCGCTCGAGCCGCTGCTGTTGTTGAGTGGTCCCTAT 228
Db 121 CCCACTGTTGTCAGGCGGGGACGCTGAGCGTGGTCCGGTGTGTTGGGAAGCCCTT 180
QY 229 AAACCTGTTGCTCACTTTCATTTTACCTTTTCCATGCTGTTTATGAGTGGTCCCTAT 286
Db 181 AAACCTGTTGCTGCTTTCATTTTAACTTTTTCATGCGGCTGAGTGGTCTTAATCTAT 238

RESULT 8
BV150853
LOCUS PZA02088-74468-CO159 Zea mays CO159 Zea mays STS 11-MAY-2004
DEFINITION tagged site.
ACCESSION BV150853
VERSION BV150853.1 GI:47100310
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 338)
McMullen,M.D., Vroh Bi,I., Schultz,L., Duru,N., Schroeder,S.S.,
Sanchez-Villeda,H., Houchins,K., Fang,Z., Polacco,M., Gardiner,J.
and Coe,E.H.Jr.
MMP SNP Discovery
Unpublished (2003)

Contact: Michael D. McMullen
Maize Mapping Project
University of Missouri-Columbia
301 Curtis Hall, Columbia, MO 65211-7020, USA
Tel: 5738827606
Fax: 5738847850
Email: McMullenM@missouri.edu
Primer A: CTATGCAATGATCTGGAACCTG
Primer B: TAAGATGGATGGGACACAAAT
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with AmpliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

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/db_xref="taxon:4577"
/clone_lib="Zea mays Mp708"
/dev_stages="seedling"
/notes="Organ: leaf; genomic DNA from inbred line"
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STTS
ORIGIN

Query Match 49.8%; Score 144.8; DB 10; Length 338;
Best Local Similarity 79.4%; Pred. No. 5.6e-29;
Matches 189; Conservative 0; Mismatches 37; Indels 12; Gaps 1;

QY 61 GCAATGTGATCGAACCTGTTCTTGGTGGCGAGCTAGTATGACTGTC----- 112
Db 1 GCAATGTGATCGAACCTGTTCTTGGTGGCGAGCTAGTATGACTGTTTATGATT 60

QY 113 -----GTCAAGTAAATTTGGGGGCTCCCGTATGAGATGCTGGCGGCAAGGCTCGGTGT 168
Db 1 GCAATGTGATCGAACCTGTTCTTGGTGGCGAGCTAGTATGACTGTC----- 112

QY 169 CCACCTCGTTTGGCGGGGGCGCTGGAGCCGCTGTTGGTGGGGAAGCCCTTT 228
Db 121 CCACCTCGTTTGGCGGGGGAGCGCTGGAGCGTGGTCCGGTGTGTGGGAAGCCCTTT 180

QY 229 AAATGTGTCATCTGCACTTACCTTTCCATCGCTGTTTATGAGTGGTCTAT 286
Db 181 AAATGTGTCGCTTGCACTTTTAACTTTTCATCGCGTTCAGTGGTCTAAATCTAT 238

RESULT 11
BV150859
LOCUS PZA02088-74481-NC7A Zea mays NC7A Zea mays STS 11-MAY-2004
DEFINITION tagged site.
ACCESSION BV150859
VERSION BV150859.1 GI:47100316
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 338)
McMullen,M.D., Vroh Bi,I., Schultz,L., Duru,N., Schroeder,S.S.,
Sanchez-Villeda,H., Houchins,K., Fang,Z., Polacco,M., Gardiner,J.
and Coe,E.H.Jr.
MMP SNP Discovery
Unpublished (2003)

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University of Missouri-Columbia
301 Curtis Hall, Columbia, MO 65211-7020, USA
Tel: 5738827606
Fax: 5738847850
Email: McMullenM@missouri.edu
Primer A: CTATGCAATGTGATCTGGAACCTG
Primer B: TAAGATGGATGGGACAGACAAAT
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with AmpliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer

Contact: Michael D. McMullen
Maize Mapping Project

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